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OM protein - protein search, using sw model

Run on: January 31, 2003, 07:39:58 ; Search time 39 Seconds

(Without alignments)
1175.339 Million cell updates/sec

Title: US-09-785-548-2

Perfect score: 1813
Sequence: 1 QMPPSPAPSTIFSGFRHG.....QMOKVLSPLMTMTMLVLR 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Minimum number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_101002:*

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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1813	100.0	344	22	AA667212
2	1802	99.4	610	22	AA667214
3	1802	99.4	610	22	AA667216
4	1656	91.3	319	22	AA641888
5	1648	90.9	319	22	AB111534
6	1646	90.8	313	22	AAE04760
7	1645	90.7	313	22	AAE04102
8	1640	90.5	313	22	AA667215
9	1640	90.5	313	22	AA667217
10	1234	68.1	363	22	AA087138

Result No.	Score	Query Match	Length	DB ID	Description
11	1234	68.1	363	22	AA019743
12	1234	68.1	363	22	ABP47963
13	573	31.6	811	23	ABG29279
14	567.5	31.3	671	23	AAE17496
15	520.5	28.7	376	22	AA693772
16	520.5	28.7	415	22	AB11731
17	515	28.4	336	22	AAE04779
18	515	28.4	348	22	AA087550
19	515	28.4	348	22	AA019852
20	515	28.4	407	22	ABP48072
21	515	28.4	407	22	AA019725
22	515	28.4	407	23	ABP47945
23	507	28.0	315	22	AA087250
24	497	27.4	708	22	ABE63195
25	459	25.3	550	22	ABE94880
26	430.5	23.7	234	22	AA087238
27	430.5	23.7	234	22	AA087541
28	430.5	23.7	234	22	AA084291
29	430.5	23.7	234	22	AA019717
30	430.5	23.7	234	22	ABP47937
31	411.5	22.7	228	21	AA602306
32	346.5	19.1	245	22	AB11754
33	291	16.1	1102	22	ABG29358
34	234.5	12.9	461	22	AA019715
35	234.5	12.9	461	23	ABP47935
36	217	12.0	280	22	ABE99077
37	215.5	11.9	422	17	AA097722
38	213.5	11.8	400	17	AA01114
39	213.5	11.8	400	20	AA083429
40	212.5	11.7	68	22	AA088519
41	212	11.7	412	18	AA025032
42	211.5	11.7	590	23	AB05693
43	211.5	11.7	590	23	AAE17499
44	211.5	11.7	906	23	AB08635
45	209	11.5	405	20	AA027275

ALIGNMENTS

RESULT 1
AA667212
ID AA667212 standard; Protein: 344 AA.
AC AA667212;
DT 13-NOV-2001 (first entry)
XX
DE Amino acid sequence of human Parkin-Associated Protein 1 (PAP1).
XX
KW Human; Parkin-Associated Protein 1; PAP1; Parkin gene;
KW neurodegenerative disease; Parkinson's disease.
XX
OS Homo sapiens.
XX
PN WO200160857-A2.
XX
PD 23-AUG-2001.
XX
PF 15-FEB-2001; 2001WO-FR00461.
XX
PR 17-FEB-2000; 2000FR-0001980.
XX
PR 18-APR-2000; 2000US-0198489.
XX
PA (AVET) AVENTIS PHARMA SA.
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
PI Koutnikova H, Brice A, Fournier A, Pradier L, Prades C;
XX Arnaud-Regaigne I, Kosier-Montus M, Corti O;
XX WPI: 2001-550047/61.
XX N-PSDB: AAH77663.

PT A new protein, designated Parkin-Associated Protein 1 (PAP1), is an
 PT interaction partner of Parkin and is useful to treat neurodegenerative
 PT pathologies including Parkinson's disease -

PS Claim 8; Page 58-60; 82pp; French.

CC The present sequence represents a human Parkin-Associated Protein 1
 CC (PAP1) protein. PAP1 is associated with the Parkin gene, which is
 CC mutated in certain forms of familial (juvenile autosomal recessive)
 CC Parkinson's disease. PAP1 has some homology with synaptotagmins.
 CC PAP1 is used to treat neurodegenerative diseases, particularly to
 CC diagnose and treat Parkinson's disease.

SQ Sequence 344 AA;

Query Match 100.0%; Score 1813; DB 22; Length 344;
 Best Local Similarity 100.0%; Pred. No. 4,5e-192;
 Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QNLPSPAPSTIFSGGFRHGLSIDSTCTEMGNPDNANVTGEIFAIHCFKTHSLEIC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 1 QNLPSPAPSTIFSGGFRHGLSIDSTCTEMGNPDNANVTGEIFAIHCFKTHSLEIC 60

QY 61 IKACKNLAYGEEKKKKNPYKTYLLPDRSSOGKRRKTVQORNTVDPTFOETLKYYQVAPAQ 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 IKACKNLAYGEEKKKKNPYKTYLLPDRSSOGKRRKTVQORNTVDPTFOETLKYYQVAPAQ 120

QY 121 LVTFQLOVSWHGLTLARVFLGEVITISLATWDFEDSTQSRFMRHPLRAKAEKYEDSVPQ 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 LVTFQLOVSWHGLTLARVFLGEVITISLATWDFEDSTQSRFMRHPLRAKAEKYEDSVPQ 180

QY 181 SNGELTVRAKLVLPSPRKLOEAGEGTDQPSLHGQLCLVLAGAKNLVPRPDGTLNSFVK 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 SNGELTVRAKLVLPSPRKLOEAGEGTDQPSLHGQLCLVLAGAKNLVPRPDGTLNSFVK 240

QY 241 CLTLPDQOKLRKSPVLRKQACPOKHSFVSGVTPAQLROSSLELTWDALEFGMNDRL 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 CLTLPDQOKLRKSPVLRKQACPOKHSFVSGVTPAQLROSSLELTWDALEFGMNDRL 300

QY 301 LGGTRLGSKGDTAVGDCSLSKLOMOKVLSPPNLTMTLVILH 344
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 LGGTRLGSKGDTAVGDCSLSKLOMOKVLSPPNLTMTLVILH 344

RESULT 2
 AAG67214
 ID AAG67214 standard; Protein: 610 AA.

AAG67214:

DT 13-NOV-2001 (first entry)

XX Amino acid sequence of human Parkin-Associated Protein 1 (PAP1).

DE Human; Parkin-Associated Protein 1; PAP1; Parkin gene;
 XX neurodegenerative disease; Parkinson's disease.

OS Homo sapiens.

PN MO200160857-A2.

PD 23-AUG-2001.

PF 15-FEB-2001; 2001WO-FR00461.

PR 17-FEB-2000; 2000FR-0001980.

PR 18-APR-2000; 2000US-0198489.

PA (AVET) AVENTIS PHARMA SA.

PI (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 PI Arnould-Reguigne I, Brice A, Fournier A, Pradier L, Prades C;

XX NPI: 2001-550047/61.
 DR N-PSDB; AAH77672.

PT A new protein, designated Parkin-Associated Protein 1 (PAP1), is an
 PT interaction partner of Parkin and is useful to treat neurodegenerative
 PT pathologies including Parkinson's disease -

PS Claim 10; Fig 9; 82pp; French.

CC The present sequence represents a human Parkin-Associated Protein 1
 CC (PAP1) protein. PAP1 is associated with the Parkin gene, which is
 CC mutated in certain forms of familial (juvenile autosomal recessive)
 CC Parkinson's disease. PAP1 has some homology with synaptotagmins.
 CC PAP1 is used to treat neurodegenerative diseases, particularly to
 CC diagnose and treat Parkinson's disease.

SQ Sequence 610 AA;

Query Match 99.4%; Score 1802; DB 22; Length 610;
 Best Local Similarity 99.4%; Pred. No. 1.9e-190;
 Matches 342; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QNLPSPAPSTIFSGGFRHGLSIDSTCTEMGNPDNANVTGEIFAIHCFKTHSLEIC 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 267 QNLPSPAPSTIFSGGFRHGLSIDSTCTEMGNPDNANVTGEIFAIHCFKTHSLEIC 326

QY 61 IKACKNLAYGEEKKKKNPYKTYLLPDRSSOGKRRKTVQORNTVDPTFOETLKYYQVAPAQ 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 327 IKACKNLAYGEEKKKKNPYKTYLLPDRSSOGKRRKTVQORNTVDPTFOETLKYYQVAPAQ 386

QY 121 LVTFQLOVSWHGLTLARVFLGEVITISLATWDFEDSTQSRFMRHPLRAKAEKYEDSVPQ 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 387 LVTFQLOVSWHGLTLARVFLGEVITISLATWDFEDSTQSRFMRHPLRAKAEKYEDSVPQ 446

QY 181 SNGELTVRAKLVLPSPRKLOEAGEGTDQPSLHGQLCLVLAGAKNLVPRPDGTLNSFVK 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 447 SNGELTVRAKLVLPSPRKLOEAGEGTDQPSLHGQLCLVLAGAKNLVPRPDGTLNSFVK 506

QY 241 CLTLPDQOKLRKSPVLRKQACPOKHSFVSGVTPAQLROSSLELTWDALEFGMNDRL 300
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 Db 507 CLTLPDQOKLRKSPVLRKQACPOKHSFVSGVTPAQLROSSLELTWDALEFGMNDRL 566

QY 301 LGGTRLGSKGDTAVGDCSLSKLOMOKVLSPPNLTMTLVILH 344
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 567 LGGTRLGSKGDTAVGDCSLSKLOMOKVLSPPNLTMTLVILH 610

RESULT 3
 AAG67216
 ID AAG67216 standard; Protein: 610 AA.

AAG67216:

DT 13-NOV-2001 (first entry)

XX Amino acid sequence of human Parkin-Associated Protein 1 (PAP1).

DE Human; Parkin-Associated Protein 1; PAP1; Parkin gene;
 XX neurodegenerative disease; Parkinson's disease.

OS Homo sapiens.

PN MO200160857-A2.

PD 23-AUG-2001.

PF 15-FEB-2001; 2001WO-FR00461.

PR 17-FEB-2000; 2000FR-0001980.

PR 18-APR-2000; 2000US-0198489.

PA (AVET) AVENTIS PHARMA SA.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX Koutnikova H, Brice A, Fournier A, Pradier L, Prades C;
PI Arnould-Reguigne I, Rosier-Montus M, Corti O;
XX MPI: 2001-550047/61.

DR N-PSDB; AAH77701.

XX A new protein, designated Parkin-Associated Protein 1 (PAP1), is an
PT interaction partner of Parkin and is useful to treat neurodegenerative
PT pathologies including Parkinson's disease -

PS Claim 10; Page 77-80; 82pp; French.

XX The present sequence represents a human Parkin-Associated Protein 1
CC (PAP1) protein. PAP1 is associated with the Parkin gene, which is
CC mutated in certain forms of familial (juvenile autosomal recessive)
CC Parkinson's disease. PAP1 has some homology with synaptotagmin.
CC PAP1 is used to treat neurodegenerative diseases, particularly to
CC diagnose and treat Parkinson's disease.

CC Sequence 610 AA;

Query Match 99.4%; Score 1802; DB 22; Length 610;
Best Local Similarity 99.4%; Pred. No. 1.9e-190;
Matches 342; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 QNLPSSPAPSTIFSGRHSLSIDSTCTMGNDNANVTGEIEFAIHYCFKTHSLEIC 60
DB 267 QNLPSSPAPSTIFSGRHSLSIDSTCTMGNDNANVTGEIEFAIHYCFKTHSLEIC 326
QY 61 IKACKNLAYEEKKKKKNPYKYTYLTPDRSSQGRKKTGVQNTVDPTFOETLKYQVAPQ 120
DB 327 IKACKNLAYEEKKKKKNPYKYTYLTPDRSSQGRKKTGVQNTVDPTFOETLKYQVAPQ 386
QY 121 LVNRQLOVSWHGLTLARVFLGEVITSLATWPEDESTTOSFRNHPLRAKAKEYEDSVQ 180
DB 387 LVNRQLOVSWHGLTLARVFLGEVITSLATWPEDESTTOSFRNHPLRAKAKEYEDSVQ 446
QY 181 SNGELTVRAKLVLPSPRRKQEAQEGTDPQSLHGOCLVVGAKNLPVRPDGTINSFVK 240
DB 447 SNGELTVRAKLVLPSPRRKQEAQEGTDPQSLHGOCLVVGAKNLPVRPDGTINSFVK 506
QY 241 CILTPDQOKLRKSPVLRKQACPQMKHSFVSGVTPAQLROSSLELTVMQALFGMDRL 300
DB 507 CILTPDQOKLRKSPVLRKQACPQMKHSFVSGVTPAQLROSSLELTVMQALFGMDRL 566
QY 301 LGSTRLGSKGDTAVGDAQSLSKLOMOKVLSPLMTDMLVLH 344
DB 567 LGSTRLGSKGDTAVGDAQSLSKLOMOKVLSPLMTDMLVLH 610

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RESULT 4
AAH41888
ID AAH41888 standard; Protein: 319 AA.

AC AAH41888;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 6819.

XX Human; noctropic; immunosuppressant; cytoskeletal; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.

XX Homo sapiens.

XX OS WO200153312-A1.
XX PN
XX

PD 26-JUL-2001.

XX 26-DEC-2000; 2000MO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX 09-JUL-2000; 2000US-0598042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0653450.

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0693036.

XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang Y, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX MPI: 2001-442253/47.

XX N-PSDB; AA161044.

XX Novel nucleic acids and polypeptides, useful for treating disorders

XX such as central nervous system injuries -

XX Example 2; SEQ ID NO 6819; 10078pp; English.

The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAH38642-AAH42213) with noctropic, immunosuppressant and cytoskeletal activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed

CC specification.

XX Sequence 319 AA;

Query Match 91.3%; Score 1656; DB 22; Length 319;
Best Local Similarity 99.1%; Pred. No. 1.1e-174;

Matches 313; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 29 CTEMGNFDNANVTGEIEFAIHYCFKTHSLEICIKACKNLAYGEEKKKKNPYKYTYLLPD 88
DB 4 CTEMGNFDNANVTGEIEFAIHYCFKTHSLEICIKACKNLAYGEEKKKKNPYKYTYLLPD 63
QY 89 RSSQGRKKTGVQNTVDPTFOETLKYQVAPQLVTRQLOVSWHGLTLARVFLGEVITIS 148
DB 64 RSSQGRKKTGVQNTVDPTFOETLKYQVAPQLVTRQLOVSWHGLTLARVFLGEVITIS 123
QY 149 LATWPEDESTTOSFRNHPLRAKAKEYEDSVQSGELTVRAKLVLPSPRRKQEAQEGTD 208
DB 124 LATWPEDESTTOSFRNHPLRAKAKEYEDSVQSGELTVRAKLVLPSPRRKQEAQEGTD 183
QY 209 QPSLHGOCLVVGAKNLPVRPDGTINSFVKGCLTLPDQOKLRKSPVLRKQACPQMKHS 268
DB 184 QPSLHGOCLVVGAKNLPVRPDGTINSFVKGCLTLPDQOKLRKSPVLRKQACPQMKHS 243
QY 269 FVFSGVTPAQLROSSLELTVMQALFGMDRLGSTRLGSKGDTAVGDAQSLSKLOMOK 328
DB 244 FVFSGVTPAQLROSSLELTVMQALFGMDRLGSTRLGSKGDTAVGDAQSLSKLOMOK 303
QY 329 VLSSPLMTDMLVLH 344
DB 304 VLSSPLMTDMLVLH 319

```

RESULT 5
 ABB1534
 ID ABB1534 standard; peptide: 319 AA.
 AC ABB1534;
 DT 11-JAN-2002 (first entry)
 XX
 XX Human granulysin-a homologue, SEQ ID NO:1904.
 DE
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antihemetic; antiarthritis; haemostatic; antiarteriosclerotic;
 KW cystostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vinegary; antilecer.
 XX
 XX Homo sapiens.
 OS
 PN MO200157188-A2.
 PD 09-AUG-2001.
 PF 05-FEB-2001; 2001MO-US03800.
 PR 03-FEB-2000; 2000US-0496914.
 XX 27-APR-2000; 2000US-0560875.
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT;
 PI
 DR WPI: 2001-457740/49.
 DR N-PSDB; ABA08778.
 XX
 PT Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer -
 CC
 CC Claim 20; Page 209; 1963pp: English.
 CC
 CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation regulatory activity; tissue growth activity;
 CC haematopoiesis regulatory activity; stem cell growth factor activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,

arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention.
 CC
 XX
 XX Sequence 319 AA;
 SQ
 Query Match 90.9%; Score 1648; DE 22; Length 319;
 Best Local Similarity 98.7%; Pred. No. 8,1e-174;
 Matches 312; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 29 CTEMGNFNNANTGTEIEPAHYCFKTHSLKICAKKNLAYGEEKKKCNPKYKTYLLPD 88
 DB 4 CTEMGNFNNANTGTEIEPAHYCFKTHSLKICAKKNLAYGEEKKKCNPKYKTYLLPD 63
 QY 89 RSSGKRKTGVORNTVDPFQETLKYQAPADLVTRQLOYSVNHGLTLARVFLGEVITIS 148
 DB 64 RSSGKRKTGVORNTVDPFQETLKYQAPADLVTRQLOYSVNHGLTLARVFLGEVITIS 123
 QY 149 LATWDFEDSTGSEFRNHPRAKAEKEDSVPOSNGELTVRAKLVLPSPRPKLQEAEGTD 208
 DB 124 LATWDFEDSTGSEFRNHPRAKADKEDSVPOSNGELTVRAKLVLPSPRPKLQEAEGTD 183
 QY 209 QPSLHGQLCLVVLGAKNLPYRDPGLNSFYKGCGLTLPDQOKLRLKSPVLRKQCPQWKHS 268
 DB 184 QPSLHGQLCLVVLGAKNLPYRDPGLNSFYKGCGLTLPDQOKLRLKSPVLRKQCPQWKHS 243
 QY 269 FVFSGYTPPAQLRSSLELTYWQDALFGMDRLGTRFLGSKGPTAVGDCASLSKLQMOK 328
 DB 244 FVFSGYTPPAQLRSSLELTYWQDALFGMDRLGTRFLGSKGPTAVGDCASLSKLQMOK 303
 QY 329 VLSSPNMLTMDTLVLH 344
 DB 304 VLSSPNMLTMDTLVLH 319
 DE
 XX
 XX RESULT 6
 XX AAE04760
 XX ID AAE04760 standard; Protein: 313 AA.
 XX AC AAE04760;
 XX DT 10-SEP-2001 (first entry)
 XX
 XX Human vesicle trafficking protein-3 (VETRP-3) protein.
 DE
 KW Human; vesicle trafficking protein-3; VETRP-3; vaccine; cystic fibrosis;
 KW glucose-galactose malabsorption syndrome; hypercholesterolaemia; goitre;
 KW diabetes mellitus; diabetes insipidus; hyperglycaemia; hypoglycaemia;
 KW Grave's disease; Cushing's disease; Addison's disease; AIDS; allergy;
 KW ulcerative colitis; gastrointestinal disorder; asthma; hay fever; gout;
 KW autoimmune disease; inflammatory disease; bowel disease; osteoporosis;
 KW multiple sclerosis; rheumatoid arthritis; psoriasis; anaemia; cancer;
 KW pancreatitis; Crohn's disease; glomerulonephritis; atherosclerosis;
 KW Goodpasture's syndrome; Hashimoto's thyroiditis; gene therapy; virucide;
 KW systemic lupus erythematosus; dermatitis; nephrotropic; antihelminthic;
 KW cerebroprotective.
 KW
 KW Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH 11..128
 FT Domain /note="C2 domain"

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FT Domain 13..69
FT /note= "Protein kinase C C2 domain"
FT Domain 26..115
FT /note= "Protein kinase C C2 domain"
FT Domain 54..79
FT /note= "C2 domain motif"
FT Domain 185..273
FT /note= "Protein kinase C C2 domain"
XX WO200146256-A2.
XX 28-JUN-2001.
XX 21-DEC-2000; 2000WO-US34919.
XX 21-DEC-1999; 99US-0172968.
XX 23-DEC-1999; 99US-0172066.
XX (INCY-) INCYTE GENOMICS INC.
XX Tang YT, Yue H, Bandman O, Hillman JL, Baughn MR, Lu DAM;
XX Azimzai Y, Yang J, Burford N, Au-Young J, Reddy R;
XX MPI: 2001-418040/44.
XX N-PSDB; AAD09373.
XX Novel human vesicle trafficking proteins useful for treating and
XX preventing vesicle trafficking disorders, autoimmune/inflammatory
XX disorders and cancers -
XX Claim 1; Page 103; 144pp; English.
XX
XX The present sequence is human vesicle trafficking protein-3 (VETRP-3)
XX or protein VETRP is used as vaccine. VETRP is useful for treating a disease
XX or condition associated with decreased expression of functional VETRP.
XX such as vesicle trafficking disorders e.g., cystic fibrosis, glucose-
XX galactose malabsorption syndrome, hypercholesterolaemia, diabetes
XX mellitus, diabetes insipidus, hyperglycaemia, hypoglycaemia, Grave's
XX disease, goitre, Cushing's disease, Addison's disease, gastrointestinal
XX disorders including ulcerative colitis, AIDS, allergies including
XX asthma, hay fever, autoimmune/inflammatory diseases including
XX inflammatory bowel disease, multiple sclerosis, rheumatoid arthritis,
XX osteoporosis, viral, bacterial, fungal, helminthic and protozoal
XX infections, psoriasis, pancreatitis, anaemia, Crohn's disease,
XX glomerulonephritis, atherosclerosis, dermatitis, Hashimoto's
XX thyroiditis, gout, Goodpasture's syndrome, systemic lupus erythematosus
XX and cancers. VETRP polynucleotides are useful in gene therapy and
XX diagnostic purposes.
XX
XX Sequence 313 AA;
XX
XX Query Match 90.8%; Score 1646; DB 22; Length 313;
XX Best Local Similarity 99.7%; Pred. No. 1.3e-173;
XX Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 32 MGNEDNANVTGEIEFAHYHCRTKSHLEICIRACKNLAYGEEKKKCNPKYKTYLLPDRSS 91
XX 1 MGNEDNANVTGEIEFAHYHCRTKSHLEICIRACKNLAYGEEKKKCNPKYKTYLLPDRSS 60
XX 92 GGRKRTGVORNTVDPTFOETLKGYAPAPOLVTRQLOVSWHMGTLARRFLEGEVILSLAT 151
XX 61 GGRKRTGVORNTVDPTFOETLKGYAPAPOLVTRQLOVSWHMGTLARRFLEGEVILSLAT 120
XX 152 WDFEDSTTQSFEMHPLRAKAEKYEDSVDSNGELTVRAKLVLSRPRKIQEAQEGTDPS 211
XX 121 WDFEDSTTQSFEMHPLRAKAEKYEDSVDSNGELTVRAKLVLSRPRKIQEAQEGTDPS 180
XX 212 LHGQLCLVYLAKKNLPVRPDGTLNSFVGCLTLPPQOKRTLSPTVLRKQACPOMKHSEVF 271
XX 181 LHGQLCLVYLAKKNLPVRPDGTLNSFVGCLTLPPQOKRTLSPTVLRKQACPOMKHSEVF 240
XX 272 SGVTFAQLROSSLELTVMQALFGMNDRLIGTRLSKSGDTAVGGDACSLSKLQWOKVLS 331
XX

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DB 241 SGVTFAQLROSSLELTVMQALFGMNDRLIGTRLSKSGDTAVGGDACSLSKLQWOKVLS 300
QY 332 SPNLMTDMLTVLH 344
DB 301 SPNLMTDMLTVLH 313
XX
XX RESULT 7
XX AAM40102
XX ID AAM40102 standard; Protein; 313 AA.
XX AAM40102;
XX 22-OCT-2001 (first entry)
XX Human polypeptide SEQ ID NO 3247.
XX
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX Homo sapiens.
XX OS
XX
XX WO200153312-A1.
XX 26-JUL-2001.
XX 26-DEC-2000; 2000WO-US34263.
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao QA, Zhou F, Goodrich R, Drmanac RT;
XX
XX MPI: 2001-442253/47.
XX N-PSDB; AAI59258.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -
XX
XX Example 5; SEQ ID NO 3247; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX the encoded polypeptides (AAM38642-AAM42213) with nootropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemia and
XX C.N.S disorders.
XX Note: The sequence data for this patent did not form part of the printed
XX specification.
XX
XX Sequence 313 AA;
XX

```

Query Match 90.7%; Score 1645; DB 22; Length 313;
 Best Local Similarity 99.7%; Pred. No. 1.7e-173;
 Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 MGNFDNANTGIEIEFAIHCFKTHSLEICIKACKNLAYGEEKKKCNPYKTYLLPDRSS 91
 DB 1 MGNFDNANTGIEIEFAIHCFKTHSLEICIKACKNLAYGEEKKKCNPYKTYLLPDRSS 60

QY 92 QGKRTGVQNRNTVDPTEFQETLKQVAPADLVTRQLOVSVNHLGTLARVFLGVIISLAT 151
 DB 61 QGKRTGVQNRNTVDPTEFQETLKQVAPADLVTRQLOVSVNHLGTLARVFLGVIISLAT 120

QY 132 WDFEDSTTQSFRRMHPRLAKAEKEDSVPSNGELTVRAKLVLSRPRKLOEAOEGTDOPS 211
 DB 121 WDFEDSTTQSFRRMHPRLAKAEKEDSVPSNGELTVRAKLVLSRPRKLOEAOEGTDOPS 180

QY 212 LHGOLCLVVLGAKNLPVRPDGTLNSFVKGCLTLPDQOKRLKSPYLKQACPOMKHSFVF 271
 DB 181 LHGOLCLVVLGAKNLPVRPDGTLNSFVKGCLTLPDQOKRLKSPYLKQACPOMKHSFVF 240

QY 272 SGVTPAQLRQSSLELTVMQDALFGMNDRLGSTRGSGDPAVGSDACSLSKLOMOKVLS 331
 DB 241 SGVTPAQLRQSSLELTVMQDALFGMNDRLGSTRGSGDPAVGSDACSLSKLOMOKVLS 300

QY 332 SPNLMTDMTTLVLH 344
 DB 301 SPNLMTDMTTLVLH 313

RESULT 8
 AAG67215
 ID AAG67215 standard; Protein: 313 AA.

AC AAG67215;
 DT 13-NOV-2001 (first entry)
 DE Amino acid sequence of human Parkin-Associated Protein 1 (PAP1).
 KW Human; Parkin-Associated Protein 1; PAP1; Parkin gene;
 KM neurodegenerative disease; Parkinson's disease.
 OS Homo sapiens.
 XX MO200160857-A2.
 XX 23-AUG-2001.

PR 15-FEB-2001; 2001MO-FR00461.
 PR 17-FEB-2000; 2000FR-0001980.
 PR 18-APR-2000; 2000US-0198489.

PA (AVENTIS PHARMA SA.
 (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 Koutnikova H, Brice A, Fournier A, Pradier L, Prades C;
 Arnould-Reguigne I, Rosier-Montus M, Corti O;
 WPI: 2001-550047/61.
 N-PSDB: AAH77673.

PT A new protein, designated Parkin-Associated Protein 1 (PAP1), is an
 PT interaction partner of Parkin and is useful to treat neurodegenerative
 PT pathologies including Parkinson's disease -
 PS Claim 10; Fig 10; 82pp; French.

CC The present sequence represents a human Parkin-Associated Protein 1
 CC (PAP1) protein. PAP1 is associated with the Parkin gene, which is
 CC mutated in certain forms of familial (juvenile autosomal recessive)
 CC Parkinson's disease. PAP1 has some homology with synaptotagmins.

CC PAP1 is used to treat neurodegenerative diseases, particularly to
 CC diagnose and treat Parkinson's disease.
 XX Sequence 313 AA;
 SQ

Query Match 90.5%; Score 1640; DB 22; Length 313;
 Best Local Similarity 99.4%; Pred. No. 6.1e-173;
 Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 32 MGNFDNANTGIEIEFAIHCFKTHSLEICIKACKNLAYGEEKKKCNPYKTYLLPDRSS 91
 DB 1 MGNFDNANTGIEIEFAIHCFKTHSLEICIKACKNLAYGEEKKKCNPYKTYLLPDRSS 60

QY 92 QGKRTGVQNRNTVDPTEFQETLKQVAPADLVTRQLOVSVNHLGTLARVFLGVIISLAT 151
 DB 61 QGKRTGVQNRNTVDPTEFQETLKQVAPADLVTRQLOVSVNHLGTLARVFLGVIISLAT 120

QY 152 WDFEDSTTQSFRRMHPRLAKAEKEDSVPSNGELTVRAKLVLSRPRKLOEAOEGTDOPS 211
 DB 121 WDFEDSTTQSFRRMHPRLAKAEKEDSVPSNGELTVRAKLVLSRPRKLOEAOEGTDOPS 180

QY 212 LHGOLCLVVLGAKNLPVRPDGTLNSFVKGCLTLPDQOKRLKSPYLKQACPOMKHSFVF 271
 DB 181 LHGOLCLVVLGAKNLPVRPDGTLNSFVKGCLTLPDQOKRLKSPYLKQACPOMKHSFVF 240

QY 272 SGVTPAQLRQSSLELTVMQDALFGMNDRLGSTRGSGDPAVGSDACSLSKLOMOKVLS 331
 DB 241 SGVTPAQLRQSSLELTVMQDALFGMNDRLGSTRGSGDPAVGSDACSLSKLOMOKVLS 300

QY 332 SPNLMTDMTTLVLH 344
 DB 301 SPNLMTDMTTLVLH 313

RESULT 9
 AAG67217
 ID AAG67217 standard; Protein: 313 AA.

AC AAG67217;
 DT 13-NOV-2001 (first entry)
 DE Amino acid sequence of human Parkin-Associated Protein 1 (PAP1).
 KW Human; Parkin-Associated Protein 1; PAP1; Parkin gene;
 KM neurodegenerative disease; Parkinson's disease.
 OS Homo sapiens.
 XX MO200160857-A2.
 XX 23-AUG-2001.

PR 15-FEB-2001; 2001MO-FR00461.
 PR 17-FEB-2000; 2000FR-0001980.
 PR 18-APR-2000; 2000US-0198489.

PA (AVENTIS PHARMA SA.
 (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 Koutnikova H, Brice A, Fournier A, Pradier L, Prades C;
 Arnould-Reguigne I, Rosier-Montus M, Corti O;
 WPI: 2001-550047/61.
 N-PSDB: AAH77702.

PT A new protein, designated Parkin-Associated Protein 1 (PAP1), is an
 PT interaction partner of Parkin and is useful to treat neurodegenerative
 PT pathologies including Parkinson's disease -
 PS Claim 10; Page 80-82; 82pp; French.

CC The present sequence represents a human Parkin-associated protein 1
CC (PAP1) protein. PAP1 is associated with the Parkin gene, which is
CC mutated in certain forms of familial (juvenile autosomal recessive)
CC Parkinson's disease. PAP1 has some homology with synaptotagmins.
CC PAP1 is used to treat neurodegenerative diseases, particularly to
CC diagnose and treat Parkinson's disease.

XX Sequence 313 AA:

Query Match 90.5%; Score 1640; DB 22; Length 313;

Best Local Similarity 99.4%; Pred. No. 6, 1e-173;

Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 32 MGNFNAVNTGELIEFAIHYCFKTHSLKICAKKNLAYGEEKKKCNPYKYTLPPDRSS 91
DB 1 MGNFDNAVNTGELIEFAIHYCFKTHSLKICAKKNLAYGEEKKKCNPYKYTLPPDRSS 60
QY 92 QGKRRKGVORNVDPFQETLKVQVAPQALVTRQLOVSWHGLTARVRLGVIISLAT 151
DB 61 QGKRRKGVORNVDPFQETLKVQVAPQALVTRQLOVSWHGLTARVRLGVIISLAT 120
DB 152 WDFEDSTTOSFPMHPLRAKAEKEDSVPSNGELTVRAKLVLPSRPRLQEAQEGTDPS 211
DB 121 WDFEDSTTOSFPMHPLRAKAEKEDSVPSNGELTVRAKLVLPSRPRLQEAQEGTDPS 180
QY 212 LHGQLCLVVLGAKNLPVRPDGTLNSFVKGCLTLPDQKLRKSPVLKQACPOWKSFEV 271
DB 181 LHGQLCLVVLGAKNLPVRPDGTLNSFVKGCLTLPDQKLRKSPVLKQACPOWKSFEV 240
QY 272 SGVTPAQRLQSSLELTVMOQALFGMNDRLIGTRLSKSGPTAVGQACSLKIQMOKVLS 331
DB 241 SGVTPAQRLQSSLELTVMOQALFGMNDRLIGTRLSKSGPTAVGQACSLKIQMOKVLS 300
QY 332 SPNLWTDMLTVLH 344
DB 301 SPNLWTDMLTVLH 313

RESULT 10
ID AAU87138 standard; Protein; 363 AA.
AC AAU87138;
XX 05-JUN-2002 (first entry)
DE Novel central nervous system protein #48.
XX Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;
XX hyperproliferative disorder; neoplasm; cardiovascular disorder;
XX cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;
XX nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;
XX acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;
XX adenocarcinoma; reproductive system disorder; testicular feminisation;
XX endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;
XX respiratory disorder; renal disorder; kidney failure; blood disorder;
XX myocardial infarction; wound healing; cell proliferation; skin aging;
XX food additive; food preservative; gene therapy.
OS Homo sapiens.
XX
XX WO200155318-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01332.
XX
XX 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
XX 24-FEB-2000; 2000US-0184664.
XX 02-MAR-2000; 2000US-0186350.
XX 16-MAR-2000; 2000US-0189874.
XX 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0228928.
PR 01-SEP-2000; 2000US-0228943.
PR 01-SEP-2000; 2000US-0228344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0233397.
PR 14-SEP-2000; 2000US-0233398.
PR 14-SEP-2000; 2000US-0233399.
PR 14-SEP-2000; 2000US-0233400.
PR 14-SEP-2000; 2000US-0234201.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235834.
PR 26-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 27-SEP-2000; 2000US-0235837.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.

Query Match	68.1%	Score 1234	DB 22	Length 363	
Best Local Similarity	97.5%	Pred. No. 8.9e-128			
Matches 234	Conservative	0	Mismatches 6	Indels 0	Gaps 0
Oy	1	ONLPSSPAPSTFFSGCFRHSLSIDSTCTEMGNPDNANVTGEIEFAHYCFKTSLEIC	60		
Db	124	ONLPSSPAPSTFFSGCFRHSLSIDSTCTEMGNPDNANVTGEIEFAHYCFKTSLEIC	183		
Oy	61	IKACKNLAYGEBKKKKCNPKYKTYLLPPRSSGKRKTVGRNTYDPTFOETLKTOVAPAQ	120		
Db	184	IKACKNLAYGEBKKKKCNPKYKTYLLPPRSSGKRKTVGRNTYDPTFOETLKTOVAPAQ	243		
Oy	121	LVTRQLQSVVHLGLTARVFLGEVYIISLAWDFEDSTQTSFRRMHLPAKAKEXEDSPQ	180		
Db	244	LVTRQLQSVVHLGLTARVFLGEVYIISLAWDFEDSTQTSFRRMHLPAKAKEXEDSPQ	303		
Oy	181	SNGELTVAKLVLPSPRKLQADQGTQPSLRGQLCLVYTGAKNLPVRPGTILNSFYKG	240		
Db	304	SNGELTVAKLVLPSPRKLQADQGTQPSXHQQLCLVYTGAKNLPVRPGTILNSFYKG	363		

RESULT 11

AAU19743

AAU19743 standard; Protein; 363 AA.

AAU19743:

06-DEC-2001 (first entry)

Human novel extracellular matrix protein, Seq ID No 393.

Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV; anti-nausea; antirheumatic; antileukemic; cardiatic; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytosaric; antialzheimers; immune/autoimmune disease; HIV infection; anaemia; human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; cancers; hyperproliferative disorder; breast neoplasia; melanoma; Alzheimer's syndrome; Gaucher's disease; neurological diseases; Kew Alzheimer's disease; Parkinson's disease; cardiovascular disorder; cardiac arrest; tachycardia; angina; infection; corneal infections; wound healing; immunogen; gene therapy; antisense; food additive.

Homo sapiens.

W0200155368-A1.

02-AUG-2001.

17-JAN-2001; 2001WO-US01348.

31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 23-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0234984.
PR 27-SEP-2000; 2000US-0235834.
PR 29-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0240961.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
PR (HUMA-) HUMAN GENOME SCI INC.
PR Rosen CA, Barash SC, Ruben SM;
PR WPI; 2001-465572/50.
PR N-PSDB; AAS31314.
PR Nucleic acid molecules encoding human secreted extracellular matrix
PR proteins, used in preventing, treating or ameliorating a disorder, e.g.
PR Alzheimer's and Parkinson's diseases and cancers -

XX Claim 11; SEQ ID NO 393; 577bp; English.

PS The invention relates to isolated nucleic acid molecules encoding
 CC novel human secreted extracellular matrix proteins (SPs). The
 CC polynucleotides and proteins are used to prevent, treat a medical
 CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,
 CC chickens or sheep. For example, disorders associated with decreased
 CC expression of SPs. The SP polynucleotide or a vector expressing them may
 CC be administered to treat diseases by gene therapy. Antisense molecules
 CC may be administered to down regulate expression of SPs by binding with
 CC the cells own genes and preventing their expression. The polynucleotides
 CC may also be used as DNA probes in diagnostic assays. The SPs may also be
 CC used as antigens to produce antibodies and to identify modulators
 CC (agonists and antagonists) of the SPs. The anti-(SP) antibodies and
 CC antagonists may also be used to down regulate expression and activity of
 CC SP and as diagnostic agents for detecting the presence of SPs in samples.
 CC The disorders include for example: Immune/autoimmune diseases (e.g. HIV
 CC (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis
 CC and multiple sclerosis), cancers and hyperproliferative disorders (e.g.
 CC melanomas, neoplasms of the breast or liver, Sezary syndrome and
 CC Gaucher's disease), neurological diseases (e.g. Alzheimer's disease,
 CC Parkinson's disease) cardiac/cerebrovascular disorders (e.g. cardiac
 CC arrest, tachycardia and angina), infections caused by bacteria, viruses
 CC and fungi and ocular disorders (e.g. corneal infections). Other uses
 CC include wound healing, maintenance of organs before transplantation.

Query Match 68.1%; Score 1234; DB 22; Length 363;

Best Local Similarity 97.5%; Pred. No. 8.9e-128; Mismatches 234; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 QNLPSSPAPSTIFSGGFRHSLISIDSTCTEKNFNDNAVTEIEFAIHYCEKTHSLC 60
 DB 124 QNLPSSPAPSTIFSGGFRHSLISIDSTCTEKNFNDNAVTEIEFAIHYCEKTHSLC 183
 QY 61 IKACKNLAYGEEKKKCKMPYKTYLLPPRSSGCKRTGQNTVPTFQETLKYQVAP 120
 DB 184 IKACKNLAYGEEKKKCKMPYKTYLLPPRSSGCKRTGQNTVPTFQETLKYQVAP 243
 QY 121 LVTRLOLVSVHGLTLARVFLGEVYIISLATWDFEDSTQSFRRHPLRAKAEKYEDSV 180
 DB 244 LVTRLOLVSVHGLTLARVFLGEVYIISLATWDFEDSTQSFRRHPLRAKAEKYEDSV 303
 QY 181 SNGELTVRAKLVLSRPKLDQAGCTDPSLHGLCLVLGAKNLPVRPDGTLNSFVK 240
 DB 304 SNGELTVRAKLVLSRPKLDQAGCTDPSLHGLCLVLGAKNLPVRPDGTLNSFVK 363

QY 12

ID ABP47963 standard; Protein; 363 AA.

AC ABP47963;

DT 23-AUG-2002 (first entry)

DE Human polypeptide SEQ ID NO 393.

XX Human; nootropic; neuroprotective; cytosolic; dermatological; vitruce;
 KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
 KW antiparkinsonian; antisickling; antianemic; antirheumatic; cancer;
 KW antihemetic; hepatotropic; cerebroprotective; antiinflammatory;
 KW antidiabetic; antidiabetic; antidiabetic; antidiabetic; antidiabetic;
 KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; nephrotropic; gene therapy; vaccine.

OS Homo sapiens.

PN US2002042386-A1.

PD 11-APR-2002.

PF 17-JAN-2001; 2001US-0764870.

XX 31-JAN-2000; 2000US-179065P.
 PR 04-FEB-2000; 2000US-180628P.
 PR 28-JUN-2000; 2000US-214886P.
 PR 07-JUL-2000; 2000US-216647P.
 PR 11-JUL-2000; 2000US-216880P.
 PR 11-JUL-2000; 2000US-217487P.
 PR 14-JUL-2000; 2000US-217496P.
 PR 14-JUL-2000; 2000US-218290P.
 PR 26-JUL-2000; 2000US-220963P.
 PR 26-JUL-2000; 2000US-220964P.
 PR 14-AUG-2000; 2000US-224518P.
 PR 14-AUG-2000; 2000US-224519P.
 PR 14-AUG-2000; 2000US-225267P.
 PR 14-AUG-2000; 2000US-225268P.
 PR 14-AUG-2000; 2000US-225270P.
 PR 14-AUG-2000; 2000US-225447P.
 PR 14-AUG-2000; 2000US-225757P.
 PR 14-AUG-2000; 2000US-225758P.
 PR 22-AUG-2000; 2000US-226868P.
 PR 30-AUG-2000; 2000US-228924P.
 PR 01-SEP-2000; 2000US-228287P.
 PR 01-SEP-2000; 2000US-229343P.
 PR 01-SEP-2000; 2000US-229344P.
 PR 01-SEP-2000; 2000US-229345P.
 PR 05-SEP-2000; 2000US-229509P.
 PR 05-SEP-2000; 2000US-229513P.
 PR 08-SEP-2000; 2000US-231413P.
 PR 21-SEP-2000; 2000US-234223P.
 PR 21-SEP-2000; 2000US-234274P.
 PR 25-SEP-2000; 2000US-234977P.
 PR 27-SEP-2000; 2000US-235834P.
 PR 29-SEP-2000; 2000US-236327P.
 PR 29-SEP-2000; 2000US-236367P.
 PR 29-SEP-2000; 2000US-236368P.
 PR 29-SEP-2000; 2000US-236369P.
 PR 29-SEP-2000; 2000US-236370P.
 PR 02-OCT-2000; 2000US-236802P.
 PR 02-OCT-2000; 2000US-237037P.
 PR 02-OCT-2000; 2000US-237038P.
 PR 02-OCT-2000; 2000US-237039P.
 PR 02-OCT-2000; 2000US-237040P.
 PR 13-OCT-2000; 2000US-239935P.
 PR 20-OCT-2000; 2000US-240960P.
 PR 20-OCT-2000; 2000US-241785P.
 PR 20-OCT-2000; 2000US-241809P.
 PR 01-NOV-2000; 2000US-244617P.
 PR 17-NOV-2000; 2000US-249299P.
 PR 08-DEC-2000; 2000US-251856P.
 PR 08-DEC-2000; 2000US-251868P.
 PR 08-DEC-2000; 2000US-251869P.
 XX
 PA (ROSE/) ROSEN C A.
 PA (RUBEN/) RUBEN S M.
 PA (BARA/) BARASH S C.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 DR MPI: 2002-470713/50.
 DR N-PSDB; AB066638.
 XX
 PT New nucleic acid encoding human proteins, useful for diagnosis,
 PT treatment and prevention of e.g. osteoporosis, also related
 PT polypeptides and antibodies
 XX
 PS Claim 11; SEQ ID NO 393; 235bp + Sequence Listing; English.

XX The invention relates to novel genes (AB06521-AB066785) and proteins
 CC (ABP47846-ABP48110) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast

CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
CC hemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases such as viral, bacterial, fungal
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html?poocid=999909764870.
XX
SQ Sequence 363 AA:
Query Match 68.1%; Score 1234; DB 23; Length 363;
Best Local Similarity 97.5%; Pred. No. 8.9e-128;
Matches 234; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 QNLSPSPAPSTIFSGFRHGLISIDSTCTEMGNFDMNAVTEIEFAIHCFKTHSLETIC 60
124 QNLSPSPAPSTIFSGFRHGLISIDSTCTEMGNFDMNAVTEIEFAIHCFKTHSLETIC 183
DB IKACKNLAYGEEKKKCKMPYKTYLLPDRSSQGRKRTGVQRNTVDPFQETTLKYQVAPAQ 120
184 IKACKNLAYGEEKKKCKMPYKTYLLPDRSSQGRKRTGVQRNTVDPFQETTLKYQVAPAQ 243
QY 121 LVTRQLOYSVWHLGLTLARVFLGEVYIISLATWDFEDSTTQSFRRMPLRAKAEKYEDSVPO 180
244 LVTRQLOYSVWHLGLTLARVFLGEVYIISLATWDFEDSTTQSFRRMPLRAKAEKYEDSVPO 303
QY 181 SNGELTVAKILVPSRPKRLQDPAOGSTDPQLHGQLCLVYLGAKNLPVRPDGTLNSFVKG 240
304 SNGELTVAKILVPSRPKRLQDPAOGSTDPQLHGQLCLVYLGAKNLPVRPDGTLNSFVKG 363
DB
RESULT 13
ABG29279 standard; Protein: 811 AA.
XX
AC ABG29279;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #29270.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX MO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX
XX N-PSDB: AAS93466.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 20; SEQ ID NO 59638; 103pp; English.

XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polynucleotide chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 811 AA:
Query Match 31.6%; Score 573; DB 22; Length 811;
Best Local Similarity 39.2%; Pred. No. 7.4e-54;
Matches 136; Conservative 57; Mismatches 132; Indels 22; Gaps 8;
QY 14 SSGFRHGLISIDSTCTEMGNFDMNAVTEIEFAIHCFKTHSLETICIKACKNLAYGEEK 73
363 ASGLSTSLNSMMSVYSTGQGNKVSCELLHISTYCKTGGLTFPKACNLAIQDCK 422
DB 74 KKKCNPYKTYLLPDRSSQGRKRTGVQRNTVDPFQETTLKYQVAPOLVTRQLOYSVWHL 133
423 KQRTDAYVYSYLLPDKSNKKRKTIRGT-NPEFNETLKYITSHQTETRLQSVWHY 481
QY 134 GTLARVFLGEVYIISLATWDFEDSTTQSFRRMPLRAKAEKYEDSVPOSGELTVAKILV 193
482 DRFRNSFLGEVYIISLATWDFEDSTTQSFRRMPLRAKAEKYEDSVPOSGELTVAKILV 538
DB 194 PSR-----PRKLO-----EAQEGTDPQLHGQLCLV-VILGAKNL-PVRPDGTLNSFVKG 241
539 PEENMLPPEQLOGNKTKTKKKKSPVYISGILEVFTKEAKNLPAVKSGLSDSVKRY 598
QY 242 LTPDQOKRLKSPVLRQACPQWKRSEFVSQVTPAOLROSSLELTWDOALFGMNDRL 301
599 LTPDQOKRLKSPVLRQACPQWKRSEFVSQVTPAOLROSSLELTWDOALFGMNDRL 657
QY 302 GGTRLGSKGTAVG-----DACSLSKIQOKVLSSPNIMTMTVL 343
658 GGTRLGSKGTAVG-----DACSLSKIQOKVLSSPNIMTMTVL 704
DB
RESULT 14
AAE17496 standard; Protein: 671 AA.
XX
AC AAE17496;
XX
XX 22-APR-2002 (first entry)
XX
XX Human secretion and trafficking protein-5 (SAT-5).
XX
XX Human; secretion and trafficking protein-5; vesicle trafficking disorder;
KW SAT-5; cystic fibrosis; diabetes mellitus; gastrointestinal disorder;
KW Grave's disease; ulcerative colitis; cardiac disorder; hypertension;
KW polymyositis; neurological disorder; Alzheimer's disease; dementia;
KW depression; epilepsy; Tourette's disorder; cell proliferative disorder;
KW cirrhosis; cancer; autoimmune disorder; inflammatory disorder; AIDS;
KW acquired immune deficiency syndrome; Addison's disease; allergy; asthma;
KW atherosclerosis; sickle cell anaemia; hyperglycaemia; transgenic animal;
KW gene therapy; hypotensive; nootropic; neuroprotective; antidepressant;

Db 115 CKNLAYGEEKKRCNPNYKTYLLPDRSSOGKRRKTRVQKNTLDPFTFEETLKYYQVDPQLMT 174
 QY 124 ROLQSVVHMLGLTARVFLGEVITISLATWDFEDSTQSRFHMHLRAKAEYEDSVPOSNG 183
 Db 175 RRLQSVVHMLGLTARVFLGEVITISLATWDFEDSTQSRFHMHLRAKAEYEDSVPOSNG 234
 QY 184 ELTVRAKLVLSRPRLQEAQEGTDPQLHGLCLVVLGAKNLPVRPDDGLNSFVAGCLT 243
 Db 235 ELAVRAKLVLPAGPRKPEAEG--QLALNGQLCLVVLGAKNLPVRSDGLNSFVAGCLT 292
 QY 244 LPDOOKLRLKSPVLAKQACPOWKHSFVSGVTPAOLROSSLELTWDAQLFGMNDRLGG 303
 Db 293 LPNOOKLRLKSPVLAKQACPOWKHSFVSGVTPAOLROSSLELTWDAQLFGMNDRLGG 352
 QY 304 TRLGSKGDTAVGDAACSLKLOMOKVLSSPNLMTMTLVH 344
 Db 353 ARLGSKGAACGCPDGSQSKLOMOKVLSSPNLMTMTLVH 393

ULT 2

099N48 PRELIMINARY; PRT; 393 AA.

AC 099N48; (Tremblrel, 17, Created)
 DT 01-JUN-2001 (Tremblrel, 17, last sequence update)
 DT 01-JUN-2001 (Tremblrel, 19, last annotation update)
 DE Synaptotagmin-like protein 3-a delta 35-II.
 GN SYTL3 OR SLP3-A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE=21226169; PubMed=11327731;
 RA Fukuda M., Saegusa C., Mikoshiba K.;
 RT "Novel splicing isoforms of synaptotagmin-like proteins 2 and 3:
 RT Identification of the SLP homology domain";
 RL Biochem. Biophys. Res. Commun. 283:513-519(2001).
 DR EMBL: AB057765; BAB41093.1; -;
 DR MGD: MGI:1933367; SYTL3.
 DR InterPro: IPR000008; C2.
 DR Pfam: PF00168; C2; 2.
 DR SMART: SM00239; C2; 2.
 DR PROSITE: PS50004; C2.DOMAIN.2; 2.
 SQ SEQUENCE 393 AA; 43755 MW; D6D27768F455E91B CRC64;

Query Match 81.1%; Score 1471; DB 11; Length 393;
 Best Local Similarity 81.8%; Pred. No. 4, 7e-131;

Matches 279; Conservative 30; Mismatches 30; Indels 2; Gaps 1;

QY 4 PSSPAPSTIFSGGFRHSLISIDSTCTEMGNFNPNAVNGEIEFAIHCFKTHSLCICIK 63
 Db 55 PSSPHTSAVSSGGLRHSLSINSTCTEMGNFNPNAVNGEIEFAIHCFKTHSLCICIK 114
 QY 64 CKNLAYGEEKKRCNPNYKTYLLPDRSSOGKRRKTRVQKNTLDPFTFEETLKYYQVDPQLMT 123
 Db 115 CKNLAYGEEKKRCNPNYKTYLLPDRSSOGKRRKTRVQKNTLDPFTFEETLKYYQVDPQLMT 174
 QY 124 ROLQSVVHMLGLTARVFLGEVITISLATWDFEDSTQSRFHMHLRAKAEYEDSVPOSNG 183
 Db 175 RRLQSVVHMLGLTARVFLGEVITISLATWDFEDSTQSRFHMHLRAKAEYEDSVPOSNG 234
 QY 184 ELTVRAKLVLSRPRLQEAQEGTDPQLHGLCLVVLGAKNLPVRPDDGLNSFVAGCLT 243
 Db 235 ELAVRAKLVLPAGPRKPEAEG--QLALNGQLCLVVLGAKNLPVRSDGLNSFVAGCLT 292
 QY 244 LPDOOKLRLKSPVLAKQACPOWKHSFVSGVTPAOLROSSLELTWDAQLFGMNDRLGG 303
 Db 293 LPNOOKLRLKSPVLAKQACPOWKHSFVSGVTPAOLROSSLELTWDAQLFGMNDRLGG 352
 QY 304 TRLGSKGDTAVGDAACSLKLOMOKVLSSPNLMTMTLVH 344

Db 353 ARLGSKGAACGCPDGSQSKLOMOKVLSSPNLMTMTLVH 393

RESULT 3

099N49 PRELIMINARY; PRT; 412 AA.

AC 099N49; (Tremblrel, 17, Created)
 DT 01-JUN-2001 (Tremblrel, 17, last sequence update)
 DT 01-JUN-2002 (Tremblrel, 21, last annotation update)
 DE Synaptotagmin-like protein 3-a + 35-I (Synaptotagmin-like 3).
 GN SYTL3 OR SLP3-A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE=21226169; PubMed=11327731;
 RA Fukuda M., Saegusa C., Mikoshiba K.;
 RT "Novel splicing isoforms of synaptotagmin-like proteins 2 and 3:
 RT Identification of the SLP homology domain";
 RL Biochem. Biophys. Res. Commun. 283:513-519(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SALIVARY GLAND;
 RA Strusberg R.;
 RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB057764; BAB41092.1; -;
 DR EMBL: BC022608; BAB22608.1; -;
 DR MGD: MGI:1933367; SYTL3.
 DR InterPro: IPR000008; C2.
 DR Pfam: PF00168; C2; 2.
 DR SMART: SM00239; C2; 2.
 DR PROSITE: PS50004; C2.DOMAIN.2; 2.
 SQ SEQUENCE 412 AA; 45954 MW; AB1EDD538CCCB218 CRC64;

Query Match 81.1%; Score 1471; DB 11; Length 412;
 Best Local Similarity 81.8%; Pred. No. 5e-131;

Matches 279; Conservative 30; Mismatches 30; Indels 2; Gaps 1;

QY 4 PSSPAPSTIFSGGFRHSLISIDSTCTEMGNFNPNAVNGEIEFAIHCFKTHSLCICIK 63
 Db 74 PSSPHTSAVSSGGLRHSLSINSTCTEMGNFNPNAVNGEIEFAIHCFKTHSLCICIK 133
 QY 64 CKNLAYGEEKKRCNPNYKTYLLPDRSSOGKRRKTRVQKNTLDPFTFEETLKYYQVDPQLMT 123
 Db 134 CKNLAYGEEKKRCNPNYKTYLLPDRSSOGKRRKTRVQKNTLDPFTFEETLKYYQVDPQLMT 193
 QY 124 ROLQSVVHMLGLTARVFLGEVITISLATWDFEDSTQSRFHMHLRAKAEYEDSVPOSNG 183
 Db 194 RRLQSVVHMLGLTARVFLGEVITISLATWDFEDSTQSRFHMHLRAKAEYEDSVPOSNG 253
 QY 184 ELTVRAKLVLSRPRLQEAQEGTDPQLHGLCLVVLGAKNLPVRPDDGLNSFVAGCLT 243
 Db 254 ELAVRAKLVLPAGPRKPEAEG--QLALNGQLCLVVLGAKNLPVRSDGLNSFVAGCLT 311
 QY 244 LPDOOKLRLKSPVLAKQACPOWKHSFVSGVTPAOLROSSLELTWDAQLFGMNDRLGG 303
 Db 312 LPNOOKLRLKSPVLAKQACPOWKHSFVSGVTPAOLROSSLELTWDAQLFGMNDRLGG 371
 QY 304 TRLGSKGDTAVGDAACSLKLOMOKVLSSPNLMTMTLVH 344
 Db 372 ARLGSKGAACGCPDGSQSKLOMOKVLSSPNLMTMTLVH 412

RESULT 4

099N54 PRELIMINARY; PRT; 607 AA.

ID 099N54; (Tremblrel, 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Synaptotagmin-like protein 3-a.
 GN SYTL3 OR SLP3-A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE=21226169; PubMed=11327731;
 RA Fukuda M., Saegusa C., Mikoshida K.;
 RT "Novel splicing isoforms of synaptotagmin-like proteins 2 and 3:
 RT Identification of the SLP homology domain".
 RL Biochem. Biophys. Res. Commun. 283:513-519(2001).
 DR EMBL; AB057758; BAB41086.1; -;
 DR MGD; MGI:1933367; SYTL3.
 DR InterPro; IPR000008; C2.
 DR Pfam; PF00168; C2; 2.
 DR SMART; SM00239; C2; 2.
 PROSITE; PS50004; C2_DOMAIN_2; 2.
 SEQUENCE 607 AA; 68567 MW; F9F404D2D77A6351 CRC64;

Query Match 81.1%; Score 1471; DB 11; Length 607;
 Best Local Similarity 81.8%; Pred. No. 8,7e-131;
 Matches 279; Conservative 30; Mismatches 30; Indels 2; Gaps 1;

QY 4 PSSPASTFTSGSGFRHGSLSIDSTCTEMGNFDNANVTGEIEFAHYCEKTHSLCICIK 63
 DB 269 PSSPTSAVFSGGLRHGSLISINSTCTEMGNFDNANVTGEIEFAHYCEKTHSLCICIK 328
 QY 64 CKNLAEGEKKKCNPKYKTYLLPDRSSQGRKRTGVQRNVTPTFOELTKQVAPQCLVT 123
 DB 329 CKNLAEGEKKKCNPKYKTYLLPDRSSQGRKRTGVQRNVTPTFOELTKQVAPQCLVT 388
 QY 124 ROLQVSMHLGTARVFLGCVIISLATWDFEDSTQSFRWHPRAKAEKEDSVPOSNG 183
 DB 389 RRLQSVNHLGTARVFLGCVIISLATWDFEDSTQSFRWHPRAKAEKEDSVPOSNG 448
 QY 184 ELTVRAKLVLPSPRRKLQEAQEGTDQPSLHGQCLVYLGAKNLPVRPDGTLNSEVKGCLT 243
 DB 449 ELTVRAKLVLPSPRRKLQEAQEGTDQPSLHGQCLVYLGAKNLPVRPDGTLNSEVKGCLT 506
 QY 244 LPDQQLRLKSPYLKQACPOKMSFVFSVTPAQLQSSLELTWQALFGMNDRLIGE 303
 DB 507 LPDQQLRLKSPYLKQACPOKMSFVFSVTPAQLQSSLELTWQALFGMNDRLIGE 566
 QY 304 TRLSKGDVAVGDACTSLKLOKQVILSSPNLMTDMLVLH 344
 DB 567 ARLGSKGAAGCPDSGSQSKLOMHRVLSPLNLTMTVLH 607

RESULT 5
 Q99N47 PRELIMINARY: PRT: 311 AA.
 AC 099N47;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Synaptotagmin-like protein 3-b + 3S-III.
 GN SYTL3 OR SLP3-B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-BRAIN;
 RX MEDLINE=21226169; PubMed=11327731;
 RA Fukuda M., Saegusa C., Mikoshida K.;
 RT "Novel splicing isoforms of synaptotagmin-like proteins 2 and 3:
 RT Identification of the SLP homology domain".

RL Biochem. Biophys. Res. Commun. 283:513-519(2001).
 DR EMBL; AB057766; BAB41094.1; -;
 DR MGD; MGI:1933367; SYTL3.
 DR InterPro; IPR000008; C2.
 DR Pfam; PF00168; C2; 2.
 DR SMART; SM00239; C2; 2.
 PROSITE; PS50004; C2_DOMAIN_2; 2.
 SEQUENCE 311 AA; 34884 MW; 91986B928DC510E0 CRC64;

Query Match 74.7%; Score 1354; DB 11; Length 311;
 Best Local Similarity 82.1%; Pred. No. 4,2e-120;
 Matches 257; Conservative 28; Mismatches 26; Indels 2; Gaps 1;

QY 32 MGNFDNANVTGEIEFAHYCEKTHSLCICAKKNLAEGEKKKCNPKYKTYLLPDRSS 91
 DB 1 MGNFDNANVTGEIEFAHYCEKTHSLCICAKKNLAEGEKKKCNPKYKTYLLPDRSS 60
 QY 92 QGRKRTGVQRNVTPTFOELTKQVAPQCLVTPTFOLOLVSMHLGTARVFLGCVIISLAT 151
 DB 61 QGRKRTGVQRNVTPTFOELTKQVAPQCLVTPTFOLOLVSMHLGTARVFLGCVIISLAT 120
 QY 152 WDFEDSTQSFRWHPRAKAEKEDSVPOSNGELTVRAKLVLPSPRRKLQEAQEGTDQPS 211
 DB 121 WDFEDSTQSFRWHPRAKAEKEDSVPOSNGELTVRAKLVLPSPRRKLQEAQEGTDQPS 178
 QY 212 LFGQCLVYLGAKNLPVRPDGTLNSEVKGCLTLPDQQLRLKSPYLKQACPOKMSFVF 271
 DB 179 LFGQCLVYLGAKNLPVRPDGTLNSEVKGCLTLPDQQLRLKSPYLKQACPOKMSFVF 238
 QY 272 SCVTPAQLQSSLELTWQALFGMNDRLIGETRLSGKGDVAVGDACTSLKLOKQVILSS 331
 DB 239 NGVSSQQLQSSLELTWQALFGMNDRLIGETRLSGKGDVAVGDACTSLKLOKQVILSS 298
 QY 332 SPNLMTDMLVLH 344
 DB 299 SPNLMTDMLVLH 311

RESULT 6
 Q8TDM5 PRELIMINARY: PRT: 730 AA.
 AC Q8TDM5;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
 DE Synaptotagmin-like protein 5.
 GN SLP5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RA Kuroda T.S., Fukuda M., Ariga H., Mikoshida K.;
 RT "Synaptotagmin-like protein 5: A novel Rab27A effector with C-terminal
 RT tandem C2 domains".
 DR Biochem. Biophys. Res. Commun. 0:0-0(2002).
 DR EMBL; AB080222; BAB88906.1; -;
 SEQUENCE 730 AA; 81522 MW; D9E0DA98880A95ED CRC64;

Query Match 31.6%; Score 573; DB 4; Length 730;
 Best Local Similarity 39.2%; Pred. No. 1,8e-45;
 Matches 136; Conservative 57; Mismatches 132; Indels 22; Gaps 8;

QY 14 SGGFRHGSLSIDSTCTEMGNFDNANVTGEIEFAHYCEKTHSLCICAKKNLAEGEKK 73
 DB 380 ASGLSTSLNSMSVSVSETGDYGNKVKVSGEILHSYCYKGTGLTFVKNCRMLATGDEK 439
 QY 74 KKKCNPKYKTYLLPDRSSQGRKRTGVQRNVTPTFOELTKQVAPQCLVTPTFOLOLVSM 133
 DB 440 KQRTDVAVYKSYLLPDKSRNKKRKTIRKGT-NPEFETLKTYTISHQLETRTLQLSVWHY 498

```
QY      134 GTLARVETGEVILSATWPFEDSTTOSFWMHNPRAAKAEKEDSVPDSNELLVPAALV 193
          | | | | | : | | | | | : | | | | | : | | | | | :
Db      499 DREGRNSLEVELEPDSMFENNTDE--WFYLQPKVERAPDIDGLQYKEGELTVLYEIP 555

QY      194 PSR-----PRKLQ-----EAQEGTDPOSLHGOLCLV-VLGAKNLV-PVRPGTLNPSFYKGC 241
          | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db      556 PEENLMMPROQLGNKTFKKKGKKKESPVISGGILEVPIREKANNLTAVKSOGTSDSFPVKGY 615

QY      242 LTLPDOOKLYRKSEVYLKQACPPMKHSFVSVSGYTPAOLROSSLETLYWDQALFGMDRL 301
          | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db      616 LLRPDSATATHHKLTLYIKKSYNPOMNHFMESGIHPDIQKWCELTITMDEAFSSN-IFL 674

QY      302 GGFPLGSKSDTAVG-----DACSLKRLQWKQVLSPNLMTDMTLV 343
          | | | | | : | | : | | : | | : | | : | | : | | : | | : | |
Db      675 GCVRLLNGSGVSHCKNVNDMMDSQEEEDRLMQKANNNGTFFPEGVLM 721
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RESULT	7
DQ66C2A	
Q96C24	PRELIMINARY; PRT; 671 AA.
DQ66C24;	
DT 01-DEC-2001 (TREMBLrel. 19, Created)	
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DE Similar to synaptotagmin-like 4.	
OS Homo sapiens (Human)	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE=UTERUS;	
RA Strausberg R.;	
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.	
DR EMBL; BC014913; AAH14913.1; -.	
DR InterPro; IPR000008; C2.	
DR InterPro; IPR003315; RP_H3A_effector.	
DR Pfam; PF00168; C2; 2.	
DR Pfam; PF02318; RP_H3A_effector; 1.	
DR PROSITE; PSS0004; C2_DOMAIN_2; 2.	
DQ SEQUENCE 671 AA; 7609 MW; CTI5211E900EAB89 CRC64;	

Query March	31.3%	Score 567.5	DB 4	Length 671
Best Local Similarity	39.4%	Pred. No. 5.2e-45		
Matches 140; Conservative	52;	Mismatches 128;	Indels 35;	Gaps 11

[illegible]

RESULT 8
Q9H4R1

ID	09H4R1	PRELIMINARY;	PRT;	491 AA.
AC	09H4R1			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	BA524D16A.2.1 (Novel protein similar to mouse grannuphlin-a) (Fragment).			
DE	BA524D16A.2.			
GN	BA524D16A.2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Wilson S.;			
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AL391688; CAC16061.1; -.			
DR	HSSP; P21707; IRSY.			
DR	InterPro; IPR000008; C2.			
DR	InterPro; IPR001565; Synaptotagmin.			
DR	Pfam; PF00168; C2; 2.			
DR	PRINTS; PR00360; C2DOMAIN.			
DR	PRINTS; PR00399; SYNAPTOTAGMN.			
DR	SMART; SM00239; C2; 2.			
DR	PROSITE; PS50004; C2_DOMAIN_2; 2.			
FT	NON_TER			
FT	1			
FT	1			
SQ	SEQUENCE	491 AA;	54991 MW;	C94FAF6A678F5E4 CRC64;
Query Match		31.2%;	Score 566.5;	DB 4; Length 491;
Best Local Similarity		39.2%;	Pred. No. 4.1e-45;	
Matches 139;	Conservative	53;	Mismatches 128;	Indels 35; Gaps 11;

QY	2	NLPSPASTTETSGCFRHSLSLIDSTCTENGNEFNNAVNTGIEFAIHCFCFTSLLEICI	61
Dd	148	SMSGSSMSTI-----GSMMSIYS---EAGDFENIFVTGRIASFSLXEOTOSTLVVHV	197
QY	62	KACKKLAAEGEKKKKKKCNVYTKYLLIPDRSSOGCKRTGOARNVDPTFOELLETUYAAPOL	121
Dd	198	KECHOLAIADEAKCKSNKYVKTYLLPDPDSROCKRTSIRKTDINLYDITLLEYPESEL	257
QY	122	VTRLOVSVMHLGTARRVFLGEVILISLATWDEFESTOSFRRHDLRAK-AEKYEDSVPO	180
Dd	258	AORLTQFVVHHGRGRNMTFLGEAFIOMDSMDLKRLDHCL--PLHAKISAESPGLPS	314
QY	181	SNGELTVASAKIYLBPR-----PRKIQAEOEGPDQSLHGOLCTLYVLGAKNL-PVPDPGL	234
Dd	315	HKGELVSLAKTIIPASKITPYVGDBRKRSKSGEG-----GELQWIKEAKNLTAAGAOTS	367
QY	235	NSFYKGCITLTPDOOK-RLKSPBLERQACPMWRHSFEVSGVTPPAQLROSSIELTVWDAL	293
Dd	368	DSFYVGYL-LPMRNKASRKRTPYMKKTILNPYHNHTFFYVNGVLELDLOMHCELTIIYWDEEP	426
QY	294	FGMNDRIILGGRIIG-----SKGDITAVGGDACSLSKLOMOKVLIASSPNLMWTDMYL	343
Dd	427	LASNQ-FLGVRFLGCGTGISMGEEVDDMDSDTEGEENVSLQKMKNQYGSNAEBGTIOL	480

RESULT	9		
09R001			
ID	09R001	PRELIMINARY;	PRT; 673 AA.
AC	09R001;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	Granuphillin-a.		
GN	SYTL4.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxID=10090;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RX	MEDLINE=99428529; PubMed=10497219;		


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RESULT 10
GRAB07
08VH07 PRELIMINARY; PRT; 672 AA.
08VH07;
01-MAR-2002 (TReMBLrel_20, Created)
01-MAR-2002 (TReMBLrel_20, Last sequence update)
01-JUN-2002 (TReMBLrel_21, Last annotation update)
GRanpuhlin A.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
RA Coppola T., Frantz C., Regazzi R.;
RT "Characterization of granpuhlin, a beta cell-specific protein.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF419341; AAL38513.1; -.
DR InterPro; IPR000008; C2.
DR InterPro; IPR003315; RPH3A_effector.
DR Pfam; PF00168; C2; 2.
DR Pfam; PF02318; RPH3A_effector; 1.
DR PRINTS; PRO0360; C2DOMAIN.
DR SMART; SM00239; C2; 2.
DR PROSITE; PS50004; C2_DOMAIN_2; 2.
SQ SEQUENCE 672 AA; 7390 MW; 0F99F4DB5202400 CRC64;

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RESULT 11		
099J90		
AC	PRELIMINARY;	PRT; 376 AA.
ID		
IT	099J90:	
RC	01-JUN-2001 (TEMBLrel. 17, Created)	
DT	01-JUN-2001 (TEMBLrel. 17, Last sequence update)	
DT	01-MAR-2002 (TEMBLrel. 20, Last annotation update)	
DE	Synaptotagmin-like protein 2-c.	
GN	SYTL2 OR SLP2-C OR SLP2.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NBBL_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-BALB/C; TISSUE-BRAIN;	
RA	Fukuda M., Saegusa C., Mikoshiba K.;	
RT	"Novel splicing isoforms of synaptotagmin-like proteins 2 and 3:	
RT	Identification of the SLP homology domain.";	
RL	Biochem. Biophys. Res. Commun. 0:0-0(2001).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-BALB/C; TISSUE-ADULT BRAIN;	
RX	MEDLINE-21139758; Pubmed-11243866;	
RA	Fukuda M., Mikoshiba K.;	
RT	"Synaptotagmin-like protein 1-3: A novel family of C-terminal-type	
RT	tandem C2 proteins.";	
RL	Biochem. Biophys. Res. Commun. 281:1226-1233(2001).	
DR	EMBL; AB057756; BAB41084.1; -.	
DR	EMBL; AB050742; BAB32652.1; -.	
DR	HSSP; P21707; IBYN.	
DR	MGD; MGI:1933366; Sytl2.	
DR	InterPro: IPR000008; C2.	
DR	InterPro: IPR001899; Gram_pos_anchor.	
DR	InterPro: IPR003880; Phantme_attach.	
DR	InterPro: IPR001565; Synaptotagmin.	
DR	Pfam; PF00168; C2; 2.	
DR	PRINTS; PR00360; C2DOMAIN.	
DR	PRINTS; PR00399; SYNAPTOAGMN.	
DR	SMART; SM00239; C2; 2.	
DR	PROSITE; PSS0004; C2_DOMAIN_2; 2.	
DR	PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.	
DR	PROSITE; PS00012; PHOSPHOANTHETHEINE; UNKNOWN_1.	
DR	SEQUENCE 376 AA; 4261 MW; BIA35979104F5816 CRC64;	

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 31, 2003, 07:39:58 ; Search time 20 Seconds
(without alignments)
1653.512 Million cell updates/sec

Title: US-09-785-548-2

Perfect score: 1813

Sequence: 1 QNLPSSPAPRTIFSGGFRHG.....OMQKVLSPNLTWDTLVH 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Search: 283224 seqs, 96134422 residues 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	12.7	511	2	S58399
2	222.5	12.3	441	2	A40707
3	220.5	12.2	439	2	JH0414
4	219	12.1	279	2	S58402
5	218	12.0	537	2	JH0415
6	217.5	12.0	424	2	I51210
7	216.5	11.9	498	2	PC6300
8	215.5	11.9	422	1	BMRT2X
9	215.5	11.9	422	1	A55417
10	213.5	11.8	386	2	I59387
11	213.5	11.8	400	2	JC2473
12	212	11.7	588	2	A53563
13	211.5	11.7	422	1	BMRT1Y
14	211.5	11.7	422	1	A45486
15	210.5	11.6	427	2	JH0413
16	207	11.4	412	2	JC4921
17	207	11.4	681	2	JX0338
18	207	11.4	684	2	I58166
19	202	11.1	704	2	A48097
20	200.5	11.1	421	2	S09595
21	199.5	11.0	315	2	T32059
22	189.5	10.5	743	2	T00634
23	189.5	10.5	1212	2	T00332
24	188.5	10.4	474	1	BMRT5Y
25	186	10.3	257	2	T16355
26	186	10.3	403	2	S33318
27	179	9.9	353	2	S58401
28	177.5	9.8	403	2	S58400
29	171	9.4	387	2	JC7398

30	171	9.4	390	2	T28967	hypothetical prote
31	170	9.4	1658	2	T42642	phosphoinositide 3
32	169	9.3	425	2	I59355	synaptotagmin IV -
33	169	9.3	1876	2	T13801	phosphoinositide 3
34	161	8.9	1634	1	JC5500	phosphoinositide 3
35	158.5	8.7	474	2	S68695	B/K protein - rat
36	151	8.3	853	2	T29736	hypothetical prote
37	149	8.2	672	1	KIHUCA	protein kinase C (
38	149	8.2	672	1	KIRTC	protein kinase C (
39	149	8.2	1553	2	KIMSCA	protein kinase C (
40	149	8.2	1553	2	T03301	rab3 effector prote
41	149	8.2	1607	2	T21982	hypothetical prote
42	148	8.2	672	1	KIRBC	protein kinase C (
43	148	8.2	1325	2	T25753	hypothetical prote
44	140	7.7	672	1	KIBOC	protein kinase C (
45	139.5	7.7	847	2	A56039	GTPase-activating

ALIGNMENTS

RESULT 1

S58399
cellulagin I syti - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 13-Aug-1999
C:Accession: S58399
R:Li, C.; Ullrich, B.; Zhang, J.Z.; Anderson, R.G.W.; Brose, N.; Suedhof, T.C.
Nature 375, 594-599, 1995
A:Title: Ca(2+)-dependent and -independent activities of neural and non-neural synapt
A:Reference number: S58399; MUID:95512080; PMID:7791877
A:Accession: S58399
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-511 <LIC>
A:Cross-references: EMBL:U20105; NID:9643653; PIDD:AAA87724.1; PTD:9643654
C:Superfamily: synaptotagmin; protein kinase C C2 region homology <KC2A>
F:224-337/Domain: protein kinase C C2 region homology <KC2A>
F:336-471/Domain: protein kinase C C2 region homology <KC2B>

Query Match 12.7%; Score 230; DB 2; Length 511;
Best Local Similarity 26.9%; Pred. No. 3.9e-12;
Matches 81; Conservative 57; Mismatches 117; Indels 46; Gaps 13;

QY	38	ANVTGEIEFAHYCKTSHSLICIRACKNLAYGEKKKC	---NPVVKYLLPDRSSQK 94
DB	228	AKSCGKINPFLRYDESEFLIVRIK	---AFDLPKACFGSSDPVKITLLPDRKC -K 281
QY	95	RRTGYQNTVDPEFQETLKYQVAPQVLRQLOVSVWHGTLARVFLGVIISLATWDF	154
DB	282	LQTRVHRTLNFTEDENHFVPEYELADRLHLVDFDRFRHDMIGEVILD -NLFEA	340
QY	155	EDSTQSEFRHPLRAKAEKYEDSVPOSNGELTVRAKVLPSRRKLQEAQEGTDPSLHG	214
DB	341	SDLSETSIW-----KDQYATSESVLDGEI -MFSICVLP	377
QY	215	QCLVYLAKKINLPVRP -DGLTNSFVAGCLTLPDQQLRLKSPVLRQAC -PQKHSTVES	272
DB	378	RLLTVIRKRNKAMDITQYSDPYKVS -LCDGRRLKRRKTKIKNTLNPNVNEATIFD	436
QY	273	GTPPOLROSSLLETFYWDQALFGMNDRLGTRLGSGKGTAVGADGACSLKLMOKVLSS	332
DB	437	-TPENMDQVSLISVMDYDRVGHNE -IIGCVKVGISAE -----GLGRDMNENLAY	466
QY	333	P 333	
DB	487	P 487	

RESULT 2
A40707
synaptotagmin - Caenorhabditis elegans
N:Alternate names: ric-2

C:Species: Caenorhabditis elegans
 C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 24-Sep-1999
 C:Accession: A40707; J16226
 R:Nonet, M.L.; Grundahl, K.; Meyer, B.J.; Rand, J.B.
 Cell 73, 1291-1305, 1993
 A:Title: Synaptic function is impaired but not eliminated in Caenorhabditis elegans mutants
 A:Reference number: A40707; MUID:93313960; PMID:8391930
 A:Accession: A40707
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-441 <NOM>
 A:Cross-references: GB:L15302; NID:g289717; PIDN:AAA28145.1; PID:g289718 R,Du, Z.
 Submitted to the EMBL Data Library, April 1996
 A:Description: The sequence of C. elegans cosmid F31E8.
 A:Reference number: Z18481
 A:Accession: J16226
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-441 <DUZ>
 A:Cross-references: EMBL:U55856; NID:g1280154; PID:g1280158; PIDN:AAA98023.1; GSPDB:GN00
 A:Experimental source: strain Bristol N2; clone F31E8
 A:Gene: snt-1
 A:Map position: 2
 A:Insertions: 39/2; 132/3; 289/3; 329/1; 373/3; 408/2
 C:Superfamily: synaptotagmin; protein kinase C C2 region homology
 C:Keywords: membrane trafficking; transmembrane protein
 F:153-266/Domain: protein kinase C C2 region homology <KC2A>
 F:286-401/Domain: protein kinase C C2 region homology <KC2B>
 Query Match 12.3%; Score 222.5; DB 2; Length 441;
 Best local similarity 25.9%; Pred. No. 1.5e-11;
 Matches 78; Conservative 55; Mismatches 115; Indels 53; Gaps 10;
 QY 42 GEIEFAIHVCRTHTSLEICIKACKNLAYGEKKKCNPNYKTYLLPDRSSOGKRTGYOR 101
 DB 161 GRIOYKLDYDFQGGQLVTVIAEDLP-GMDMSGTSDPYKTLVLPERRK-KVETKYNR 217
 QY 102 NTVPDFOETLKYQVAPQALVTRQLOVSVMLGTLARVVLGEVITISLATWFEEDSTQS 161
 DB 218 KTLNPFVETETFLKAFNEDITAKTLVFAIYDPRFSKHQDIOGVLLPDKID----- 269
 QY 162 FRWHPRLAKAEKYEDSV-----QNSGELTVRAKLVLPSPRKLQEAQEGTDPSLH 213
 DB 270 -----LGAVIEEMKDIAPPPDDKEAKESLGDICFSLRYV-----PTA- 306
 QY 214 GQLLVNLGAKNLPVRPPTGLNS-FYKGCGLTLPDQOKLRKSPYLKQACPOMKHSYFS 272
 DB 307 GKLTVNLLEAKNLMKMDVGGSLDPYKTVLMQGGKRLKKRTSIKCTLNPYNSESFSFE 366
 QY 273 GVPTRALROSSLELTVMPDQALFGMDRLLGTRLGSKGDTAVGADACSLKLOMKVLSS 332
 DB 367 -VPEEQIOKVLMTVMYDKIGSMD-AIGRCLLGCGNGA-----ELRHMDMLAS 416
 QY 333 P 333
 DB 417 P 417
 RESULT 3
 JH0414
 synaptotagmin o-p65-B - electric ray (Discopyge omata)
 N:Alternate names: synaptic vesicle protein o-p65-B
 C:Species: Discopyge omata
 C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 13-Aug-1999
 A:Accession: JH0414; P50223
 C:Wendland, B.; Miller, K.G.; Schilling, J.; Scheller, R.H.
 Neuron 6, 993-1007, 1991
 A:Title: Differential expression of the p65 gene family.
 A:Reference number: JH0413; MUID:91273991; PMID:2054189
 A:Accession: JH0414
 A:Molecule type: mRNA

A:Residues: 1-439 <MEN>
 A:Cross-references: GB:M64276; NID:g213110; PIDN:AAA49228.1; PID:g213111
 A:Experimental source: electric organ
 A:Accession: P50223
 A:Molecule type: protein
 A:Residues: 'MLV', 26-34; 'XX', 194-199, 'X', 201-206; 'Y', 322-332, 'D', 334-337 <MEN1>
 C:Superfamily: synaptotagmin; protein kinase C C2 region homology
 C:Keywords: glycoprotein; membrane protein; synaptic vesicle
 F:75-101/Domain: hydrophobic <HYD>
 F:153-266/Domain: protein kinase C C2 region homology <KC2A>
 F:284-399/Domain: protein kinase C C2 region homology <KC2B>
 F:6/46/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 12.2%; Score 220.5; DB 2; Length 439;
 Best local similarity 26.2%; Pred. No. 2.2e-11;
 Matches 77; Conservative 58; Mismatches 118; Indels 41; Gaps 12;
 QY 42 GEIEFAIHVCRTHTSLEICIKACKNLAYGEKKKCNPNYKTYLLPDRSSOGKRTGYOR 101
 DB 161 GKIOFSLDYDFQANQOLTVGIIQAAELP-ALDMGSGTSDPYKTVFLPDKK-KVETKYOK 217
 QY 102 NTVPDFOETLKYQVAPQALVTRQLOVSVMLGTLARVVLGEVITISLATWFEEDSTQS 161
 DB 218 KTLNPFVETETFLKAFNEDITAKTLVFAIYDPRFSKHQDIOGVLLPDKID----- 274
 QY 162 FRWHPRLAKAEKYEDSVQNSGELTVRAKLVLPSPRKLQEAQEGTDPSLHQLCLVYL 221
 DB 275 EEMRDLDS-AEKDE--PEKLGIDCTSLRYV-----PTA-GKLTVCIL 312
 QY 222 GAKNLPVRPPTGLNS-FYKGCGLTLPDQOKLRKSPYLKQAC-POMKHSFVSGVTPAOL 279
 DB 313 EAKNLMKMDVGGSLDPYKTVLH-LQNGKRLKKRTTYVKNLNPYNSESFSFE-IPFEQI 370
 QY 280 RQSLLELTVMDQALFGMDRLLGTRLGSKGDTAVGADACSLKLOMKVLSPP 333
 DB 371 QKYOVCVTVLDYDKIKGNDAI-----GKIFVSNASGTELRHMDMLANP 415
 RESULT 4
 S58402
 synaptotagmin V - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 12-Feb-1998 #sequence_revision 15-May-1998 #text_change 13-Aug-1999
 A:Accession: S58402
 R:Li, C.; Ullrich, B.; Zhang, J.Z.; Anderson, R.G.W.; Brose, N.; Suedhof, T.C.
 Nature 375, 594-599, 1995
 A:Title: Ca(2+)-dependent and -independent activities of neural and non-neural synapt
 A:Reference number: S58399; MUID:95312080; PMID:7791877
 A:Accession: S58402
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-279 <LIC>
 A:Cross-references: EMBL:U20108; NID:g643659; PIDN:AAA87726.1; PID:g643660
 C:Superfamily: synaptotagmin; protein kinase C C2 region homology
 C:Keywords: glycoprotein; membrane trafficking; phospholipid binding; synaptic vesicle
 F:1-115/Domain: protein kinase C C2 region homology <KC2>
 F:134-249/Domain: protein kinase C C2 region homology <KC2B>
 Query Match 12.1%; Score 219; DB 2; Length 279;
 Best local similarity 25.5%; Pred. No. 1.6e-11;
 Matches 77; Conservative 48; Mismatches 139; Indels 38; Gaps 9;
 QY 33 GNFDAVNGEIEFAIHVCRTHTSLEICIKACKNLAYGEKKKCNPNYKTYLLPDRSSQ 92
 DB 1 GRRSNKACGKTLNFIKTCDDLEQLIVKIKAVLP-AKDPSSGSDPYKTYLLPDKRT- 58
 QY 93 GKRKTGVQNTVDPTEQETLKYQVAPQALVTRQLOVSVMLGTLARVVLGEVITISLATW 152
 DB 59 -KHQIKVHRKTLNPFVDEVELFPVHYNDLBARKLHFSVYDPRFSRDLIQGVVD-HFF 116
 QY 153 PDEDSTQSFRRWHPRLAKAEKYEDSVQNSGELTVRAKLVLPSPRKLQEAQEGTDPSL 212
 DB 117 DLADPPRECILW-----KQIEVYTNQNVLDGEL-MFSLCYLPTA----- 154

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OM protein - protein search, using sw model

Run on: January 31, 2003, 07:39:58 ; Search time 34 Seconds

(without alignments)
419,643 Million cell updates/sec

Title: US-09-785-548-2

Perfect score: 1813
Sequence: 1 QNLSPSPAPSTIFSGGFRHG.....QMKVLSPNLTMDTLVLH 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	222.5	12.3	441	1	SYT1_CAEEL P34693 caenorhabdi
2	220.5	12.2	439	1	SYT2_DISOM P24506 discoppyge o
3	218.5	12.1	432	1	SYT2_MOUSE P46097 mus musculu
4	218	12.0	537	1	SYT3_DISOM P24507 discoppyge o
5	217.5	12.0	424	1	SYT1_CHICK P47191 gallus gall
6	216.5	11.5	498	1	SYT1_RAT P008625 rattus norv
7	215.5	11.9	422	1	SYT2_RAT P29101 rattus norv
8	214.5	11.8	587	1	SYT3_MOUSE P35681 mus musculu
9	213.5	11.8	386	1	SYT5_RAT P47861 rattus norv
10	212.5	11.7	523	1	SYT5_RAT P47861 rattus norv
11	212	11.7	588	1	SYT3_RAT P40748 rattus norv
12	211.5	11.7	421	1	SYT1_MOUSE P46096 mus musculu
13	211.5	11.7	422	1	SYT1_BOVIN P48018 bos taurus
14	211.5	11.7	422	1	SYT1_HUMAN P21579 homo sapien
15	211.5	11.7	590	1	SYT3_HUMAN P21579 homo sapien
16	210.5	11.6	386	1	SYT5_MOUSE P47861 mus musculu
17	210.5	11.6	427	1	SYT5_MOUSE P24505 discoppyge o
18	207.5	11.4	386	1	SYT5_HUMAN P00445 homo sapien
19	207	11.4	681	1	RP3A_MOUSE P47708 mus musculu
20	207	11.4	681	1	RP3A_MOUSE P47708 mus musculu
21	204	11.3	694	1	RP3A_MOUSE P47708 mus musculu
22	204	11.3	694	1	RP3A_MOUSE P47708 mus musculu
23	202.5	11.2	426	1	SYT6_APICA P41823 aplysia cal
24	202	11.1	704	1	RP3A_BOVIN P00846 bos taurus
25	189.5	10.5	402	1	SYT7_HUMAN P43581 homo sapien
26	188.5	10.4	471	1	SYT5_DROME P21521 drosophila
27	186	10.3	431	1	SYT8_HUMAN P09188 homo sapien
28	181	10.0	430	1	SYT8_MOUSE P09188 mus musculu
29	179	9.9	385	1	SYT8_MOUSE P09188 mus musculu
30	178.5	9.8	403	1	SYT7_MOUSE P09188 mus musculu
31	176.5	9.7	425	1	SYT4_HUMAN P09188 mus musculu
32	176	9.7	430	1	SYT4_HUMAN P09188 mus musculu
33	169	9.3	425	1	SYT4_RAT P52332 rattus norv

34	164	9.0	425	1	SYT4_MOUSE	P40749 mus musculu
35	161	8.9	1634	1	PK3B_HUMAN	P00750 homo sapien
36	149	8.2	672	1	KPCA_HUMAN	P17252 homo sapien
37	149	8.2	672	1	KPCA_RAT	P05696 rattus norv
38	148	8.2	672	1	KPCA_RABIT	P10102 oryctolagus
39	140	7.7	672	1	KPCA_BOVIN	P04409 bos taurus
40	139.5	7.7	672	1	KPCA_MOUSE	P03713 rattus norv
41	139	7.7	672	1	KPCA_MOUSE	P20444 mus musculu
42	139	7.7	849	1	RS62_HUMAN	P15283 homo sapien
43	136.5	7.5	1021	1	YP77_CAEEL	P41885 caenorhabdi
44	131	7.2	2083	1	DYSE_MOUSE	P05437 mus musculu
45	127	7.0	639	1	KPCI_DROME	P05130 drosophila

ALIGNMENTS

RESULT 1
SYT1_CAEEL
ID SYT1_CAEEL STANDARD: PRT: 441 AA.
AC P34693;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Synaptotagmin I.
GN SNT-1 OR F31E8.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=93313960; PubMed=8391930;
RA Nonet M.L., Grundahl K., Meyer B.J., Rand J.B.;
RT "Synaptic function is impaired but not eliminated in C. elegans
mutants lacking synaptotagmin.";
RL Cell 73:1291-1305(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Du Z.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS
DURING TRAFFICKING OF SYNAPTIC VESICLES AT THE ACTIVE ZONE OF THE
SYNAPSE. IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT
REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL
BACKBONE (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: SYNAPTIC VESICLES AND VESICLE-LIKE
STRUCTURES.
CC -I- TISSUE SPECIFICITY: LOCALIZED TO REGIONS KNOWN TO BE RICH IN
SYNAPSES AND APPEARS TO BE ASSOCIATED WITH SYNAPTIC VESICLES.
CC ALSO FOUND IN SOME NONNEURONAL SECRETORY STRUCTURES.
CC -I- DISEASE: MUTANTS EXHIBIT SEVERE BEHAVIORAL ABNORMALITIES THAT ARE
CHARACTERISTIC OF DEFICIENCIES IN SYNAPTIC FUNCTIONS, INCLUDING
SEVERE LOCOMOTION, FEEDING, AND DEFECTION DEFECTS.
CC -I- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
CC -I- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@sib-sib.ch).
CC -----
DR EMBL: L15302; AAA28145.1; -;
DR EMBL: U55856; AAA98023.1; -;
DR PTR: A40707; A40707.
DR HSSP: P21707; IRSY.
DR WormPep: F31E8.2; CE02711.
DR InterPro: IPR000008; C2.

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DR InterPro: IPR002149; LRI.
DR InterPro: IPR001565; Synaptotagmin.
DR Pfam: PF00168; C2; 2.
DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR00389; SYNAPTOTAGM.
DR SMART: SM00239; C2; 2.
DR PROSITE: PS00499; C2_DOMAIN_1; 2.
DR PROSITE: PS00004; C2_DOMAIN_2; 2.
DR Transmembrane: Repeat; Synapse: Glycoprotein.
KM DOMAIN 1 69 VESICULAR (POTENTIAL).
FT TRANSMEM 70 96 POTENTIAL.
FT DOMAIN 97 441 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 175 262 C2 DOMAIN 1.
FT DOMAIN 306 397 C2 DOMAIN 2.
SQ SEQUENCE 441 AA; 49904 MW; F8D174337EB472DB CRC64;

Query Match 12.3%; Score 222.5; DB 1; Length 441;
Best Local Similarity 25.9%; Pred. No. 2,6e-12;
Matches 78; Conservative 55; Mismatches 115; Indels 53; Gaps 10;

42 GEIEFAIHVCFKTHSLICIKACKNLAYGEKKKCNPVYKTYLLPDRSSQGRKRGVOR 101
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
161 GRIQYKLDYDFQAGLTLYVIAQAEELP-GMDMGSTSDPYKLYLLPEKK--KYETKYHR 217
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
102 NTVDPTFOETLKYQVAPADLVTRQLOVSWHLGTLARVFLGEVIISLATWDFEDSTQOS 161
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
218 KTLNLFVNETFEFKAFNFTAKTLVFAIDPFRSKHDOIGVLIPLGKID----- 269
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
162 FRWHPRLAKAEKYEEDSV-----QSNGLVYRAKVLVPSRPRKQLQEAQEGTDQPSLH 213
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
270 -----LGAVIEEMKDLAPPPDDKEAKESLDDICFSLRYV-----PTA- 306
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
214 GOLCLVLGAKNLVPRPDGTLNS-FVKGCLTLPPDOOKLRKSPYLKQACPQMKHSFVFS 272
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
307 GKLYVILEAKNLKKMDVGLSPYKIVLMQGGKRLKKTKTSIKKLTNLNYNESFSEFE 366
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
273 GVTAPQLQSSLELTVWDALFGMNDRLGSTRGSGDPAVGGDACSLSKLQMKVLS 332
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
367 -VPEFOIKVSLMTVMYDKLGSND-AIGRCLLGGMGTA-----ELRHWMMDLAS 416
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 333 P 333
QY 417 P 417
Db

RESULT 2
SY62_DISOM STANDARD; PRT; 439 AA.
ID SY62_DISOM STANDARD; PRT; 439 AA.
P24506;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
DE Synaptotagmin B (Synaptic vesicle protein O-p65-B).
P65-B.
OS Disocpyge ommata (Electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalea; Hynnosqualea; Plistorojea; Batoidae;
OC Torpediniformes; Narcinoidei; Narcinidae; Disocpyge.
OX NCBI_TaxID=7785;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RA MEDLINE=91273991; Pubmed=2054189;
RA Wendland B., Miller K.G., Schilling J., Scheller R.H.;
RT "Differential expression of the p65 gene family.";
RT Neuron 6:993-1007(1991).
-!- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS
CC DURING TRAFFICKING OF SYNAPTIC VESICLES AT THE ACTIVE ZONE OF THE
CC SYNAPSE. IT BINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT
CC REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL
CC BACKBONE.
CC -!- SUBUNIT: HOMODIMER OR HOMOTRIMER (POSSIBLE).
CC -!- SUBCELLULAR LOCATION: SYNAPTIC VESICLES IN NEURONS.
CC -!- TISSUE SPECIFICITY: SPINAL CORD, BRAINSTEM, MIDBRAIN AND ELECTRIC

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CC ORGAN.
CC -!- SIMILARITY: CONTAINS 2 C2 DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE SYNAPTOTAGMIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M64276; AAA49228.1; -.
DR PIR: JH0414; JH0414.
DR HSSP: P21707; 1BYN.
DR InterPro: IPR000008; C2.
DR InterPro: IPR002149; LRI.
DR InterPro: IPR001565; Synaptotagmin.
DR Pfam: PF00168; C2; 2.
DR PRINTS: PR00360; C2DOMAIN.
DR PRINTS: PR00389; SYNAPTOTAGM.
DR SMART: SM00239; C2; 2.
DR PROSITE: PS00499; C2_DOMAIN_1; 2.
DR PROSITE: PS00004; C2_DOMAIN_2; 2.
KW Transmembrane; Repeat; Synapse; Multigene family; Glycoprotein.
FT TRANSMEM 1 74 VESICULAR (POTENTIAL).
FT DOMAIN 75 101 POTENTIAL.
FT DOMAIN 102 439 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 153 399 PHOSPHOLIPID BINDING (PROBABLE).
FT DOMAIN 173 262 C2 DOMAIN 1.
FT DOMAIN 304 395 C2 DOMAIN 2.
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 439 AA; 49278 MW; 2033F05FD8C6F93 CRC64;

Query Match 12.2%; Score 220.5; DB 1; Length 439;
Best Local Similarity 26.2%; Pred. No. 3,9e-12;
Matches 77; Conservative 58; Mismatches 118; Indels 41; Gaps 12;

42 GEIEFAIHVCFKTHSLICIKACKNLAYGEKKKCNPVYKTYLLPDRSSQGRKRGVOR 101
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
161 GRIQYKLDYDFQAGLTLYVIAQAEELP-ALDMGGSIDPYKLYLLPEKK--KYETKYHR 217
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
102 NTVDPTFOETLKYQVAPADLVTRQLOVSWHLGTLARVFLGEVIISLATWDFEDSTQOS 161
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
218 KTLNLFVNETFEFKAFNFTAKTLVFAIDPFRSKHDOIGVLIPLGKID----- 274
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
162 FRWHPRLAKAEKYEEDSV-----QSNGLVYRAKVLVPSRPRKQLQEAQEGTDQPSLH 221
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
275 EEWRLDES-AEKDE--PEKLGIDICTSLRYV-----PTA-GKLYVCL 312
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
222 GAKNLVPRPDGTLNS-FVKGCLTLPPDOOKLRKSPYLKQAC-PQMKHSFVSGVTPAQL 279
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
313 EAKNLKKMDVGLSDPYKLYLH-LQNGKRLKKTKTYAKKNTLNPNYNSFSEFE-IPFDOI 370
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 280 ROSSLELTVWDALFGMNDRLGSTRGSGDPAVGGDACSLSKLQMKVLS 333
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 371 QKQVQCVTVLDYDKIGKNDAL-----GKLYVGSNASTELRHWMMDLANP 415
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db

RESULT 3
SYT2_MOUSE STANDARD; PRT; 422 AA.
ID SYT2_MOUSE STANDARD; PRT; 422 AA.
P46097;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
DE Synaptotagmin II (SytlII).
GN SYT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```

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OM protein - protein search, using sw model

Run on: January 31, 2003, 07:41:42 ; Search time 197 Seconds
(without alignments)
35.236 Million cell updates/sec

Title: US-09-785-548-2
Perfect score: 1813
Sequence: 1 QNLPSPAPSTIFSGFRHSG.....QWQVLSPLNLTMDTLVH 344

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA.*
1: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1813	100.0	344	9 US-09-785-548-2	Sequence 2, Appl1
2	1802	99.4	610	9 US-09-785-548-13	Sequence 13, Appl1
3	1802	99.4	610	9 US-09-785-548-43	Sequence 43, Appl1
4	1640	90.5	313	9 US-09-785-548-15	Sequence 15, Appl1
5	1640	90.5	313	9 US-09-785-548-45	Sequence 45, Appl1
6	1234	68.1	363	10 US-09-764-870-393	Sequence 393, Appl
7	515	28.4	348	10 US-09-764-870-393	Sequence 502, Appl
8	515	28.4	407	10 US-09-764-870-375	Sequence 375, Appl
9	430.5	23.7	234	10 US-09-764-870-367	Sequence 367, Appl
10	234.5	12.9	461	10 US-09-764-870-365	Sequence 365, Appl
11	208.5	11.5	295	10 US-09-764-870-364	Sequence 364, Appl
12	194.5	10.7	140	10 US-09-867-550-790	Sequence 790, Appl
13	186	10.3	179	10 US-09-764-870-360	Sequence 360, Appl
14	182	10.0	206	10 US-09-764-870-495	Sequence 495, Appl
15	181.5	10.0	293	10 US-09-935-390A-22	Sequence 22, Appl1
16	174	9.6	1686	12 US-10-092-219-2	Sequence 2, Appl1
17	149	8.2	672	8 US-08-681-219-29	Sequence 29, Appl1
18	148.5	8.2	267	10 US-09-764-870-359	Sequence 359, Appl
19	140	7.7	208	10 US-09-764-870-497	Sequence 497, Appl

20	138.5	7.6	836	10 US-09-925-301-1088	Sequence 1088, App
21	136.5	7.5	54	10 US-09-864-761-48954	Sequence 48954, A
22	134	7.4	59	10 US-09-864-761-37895	Sequence 37895, A
23	121	6.7	136	10 US-09-764-870-372	Sequence 372, App
24	118.5	6.5	185	10 US-09-764-870-494	Sequence 494, App
25	113.5	6.3	219	10 US-09-925-300-1448	Sequence 1448, App
26	111.5	6.2	68	10 US-09-864-761-42185	Sequence 42185, A
27	91	5.0	910	10 US-09-935-868-28	Sequence 28, Appl1
28	88.5	4.9	140	10 US-09-764-870-358	Sequence 358, App
29	87.5	4.8	1193	12 US-10-040-919-2	Sequence 2, Appl1
30	87	4.8	188	10 US-09-764-870-368	Sequence 368, App
31	87	4.8	299	10 US-09-764-870-388	Sequence 388, App
32	85	4.7	1239	12 US-10-007-805-577	Sequence 577, App
33	84.5	4.7	95	10 US-09-822-635-8	Sequence 8, Appl1
34	84.5	4.7	95	10 US-09-800-971-10	Sequence 10, Appl1
35	84.5	4.7	95	10 US-09-927-112-9	Sequence 9, Appl1
36	84.5	4.7	95	10 US-09-908-664-12	Sequence 12, Appl1
37	84.5	4.7	95	10 US-09-908-664-21	Sequence 21, Appl1
38	84	4.6	756	10 US-09-844-988-9	Sequence 9, Appl1
39	84	4.6	756	10 US-09-796-872-15	Sequence 15, Appl1
40	84	4.6	756	10 US-09-771-161A-232	Sequence 232, App
41	84	4.6	756	10 US-09-844-908-9	Sequence 9, Appl1
42	83	4.6	240	9 US-10-114-893-102	Sequence 102, App
43	83	4.6	262	9 US-10-114-893-318	Sequence 318, App
44	82	4.5	507	9 US-10-037-667-3	Sequence 3, Appl1
45	80.5	4.4	465	10 US-09-969-515-12	Sequence 12, Appl1

ALIGNMENTS

RESULT 1
US-09-785-548-2
Sequence 2, Application US/09785548
Patent No. US2002015577A1
GENERAL INFORMATION:
TITLE OF INVENTION: AVENTIS PHARMACEUTICALS, INC.
FILE REFERENCE: ST00005
CURRENT APPLICATION NUMBER: US/09/785, 548
CURRENT FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 2
LENGTH: 344
TYPE: PRT
ORGANISM: Homo sapiens
US-09-785-548-2

Query Match 100.0% Score 1813; DB 9; Length 344;
Best Local Similarity 100.0%; Pred. No. 2.9e-177;
Matches 344; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	QNLPSPAPSTIFSGFRHSGLSIDSTCTEMGNEDNANTGEIEFAIHCFKTHSEIC	60
DB	1	QNLPSPAPSTIFSGFRHSGLSIDSTCTEMGNEDNANTGEIEFAIHCFKTHSEIC	60
QY	61	IRACKNLANGEKKKCNPKYKTYLLPDRSSQGRKRGVQNTYDPFOETLKKQVAPAQ	120
DB	61	IRACKNLANGEKKKCNPKYKTYLLPDRSSQGRKRGVQNTYDPFOETLKKQVAPAQ	120
QY	121	LYTRQLOVSWHKGTLARRVFLGVIISLATWPDSTDSFRHNPTRAKAEKEDSVQ	180
DB	121	LYTRQLOVSWHKGTLARRVFLGVIISLATWPDSTDSFRHNPTRAKAEKEDSVQ	180
QY	181	SNGLTYRAKLVPSRPRKLOEAOEGTDPSSLHGQLCLVYLGAKNLPVRDGTLSNFEVG	240
DB	181	SNGLTYRAKLVPSRPRKLOEAOEGTDPSSLHGQLCLVYLGAKNLPVRDGTLSNFEVG	240
QY	241	CLTLPDQOKRLKSPVLRKACQWKHSFVSGVTPAOLROSSLETLVWDALFGMDRL	300
DB	241	CLTLPDQOKRLKSPVLRKACQWKHSFVSGVTPAOLROSSLETLVWDALFGMDRL	300

OY 301 LGTRLSKGDPTAVGGDACSLSKLOMOKVLSPLNMTDMLVLH 344
 Db 301 LGTRLSKGDPTAVGGDACSLSKLOMOKVLSPLNMTDMLVLH 344

RESULT 2

US-09-785-548-13
 ; Sequence 13, Application US/09785548
 ; Patent No. US20020155577A1
 ; GENERAL INFORMATION:
 ; APPLICANT: AVENTIS PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF PARK
 ; FILE REFERENCE: ST00005
 ; CURRENT APPLICATION NUMBER: US/09/785,548
 ; CURRENT FILING DATE: 2001-02-20
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 610
 ; TYPE: PRN
 ; ORGANISM: Homo sapiens
 09-785-548-13

Query Match 99.4%; Score 1802; DB 9; Length 610;
 Best Local Similarity 99.4%; Pred. No. 8.9e-176;
 Matches 342; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ONLPSPAPSTIFSGFRRGSLISIDSTCTEMGNPNANVTGEIEFAIHCFKTHSLEIC 60
 Db 267 ONLPSPAPSTIFSGFRRGSLISIDSTCTEMGNPNANVTGEIEFAIHCFKTHSLEIC 326
 OY 61 IKACKNLAYGEEKKKKCNPYKTYLLPDRSSSGKRTGVQRTNVDPTFOETLKYQVAPAQ 120
 Db 327 IKACKNLAYGEEKKKKCNPYKTYLLPDRSSSGKRTGVQRTNVDPTFOETLKYQVAPAQ 386
 OY 121 LVTRLOLVSVHMLGLTARVFLGEVYIISLATWDFEDSTQSRFMRHLRAKAEKEDSVPO 180
 Db 387 LVTRLOLVSVHMLGLTARVFLGEVYIISLATWDFEDSTQSRFMRHLRAKAEKEDSVPO 446
 OY 181 SNGELTVRAKLVLPSPRKLQEAQEGTDQPSLHGOLCLVILAKNLPVRPDGTLNSFVGK 240
 Db 447 SNGELTVRAKLVLPSPRKLQEAQEGTDQPSLHGOLCLVILAKNLPVRPDGTLNSFVGK 506
 OY 241 CLTLPDQOKLRLKSPVLRKQACPOWKHSFVSGVTPAOLROSSLLELTVWDQALFGMNDRL 300
 Db 507 CLTLPDQOKLRLKSPVLRKQACPOWKHSFVSGVTPAOLROSSLLELTVWDQALFGMNDRL 566
 OY 301 LGTRLSKGDPTAVGGDACSLSKLOMOKVLSPLNMTDMLVLH 344
 Db 567 LGTRLSKGDPTAVGGDACSLSKLOMOKVLSPLNMTDMLVLH 610

RESULT 3

US-09-785-548-43
 ; Sequence 43, Application US/09785548
 ; Patent No. US20020155577A1
 ; GENERAL INFORMATION:
 ; APPLICANT: AVENTIS PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF PARK
 ; FILE REFERENCE: ST00005
 ; CURRENT APPLICATION NUMBER: US/09/785,548
 ; CURRENT FILING DATE: 2001-02-20
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 43
 ; LENGTH: 610
 ; TYPE: PRN
 ; ORGANISM: Homo sapiens
 US-09-785-548-43

Query Match 99.4%; Score 1802; DB 9; Length 610;
 Best Local Similarity 99.4%; Pred. No. 8.9e-176;
 Matches 342; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ONLPSPAPSTIFSGFRRGSLISIDSTCTEMGNPNANVTGEIEFAIHCFKTHSLEIC 60
 Db 267 ONLPSPAPSTIFSGFRRGSLISIDSTCTEMGNPNANVTGEIEFAIHCFKTHSLEIC 326
 OY 61 IKACKNLAYGEEKKKKCNPYKTYLLPDRSSSGKRTGVQRTNVDPTFOETLKYQVAPAQ 120
 Db 327 IKACKNLAYGEEKKKKCNPYKTYLLPDRSSSGKRTGVQRTNVDPTFOETLKYQVAPAQ 386
 OY 121 LVTRLOLVSVHMLGLTARVFLGEVYIISLATWDFEDSTQSRFMRHLRAKAEKEDSVPO 180
 Db 387 LVTRLOLVSVHMLGLTARVFLGEVYIISLATWDFEDSTQSRFMRHLRAKAEKEDSVPO 446
 OY 181 SNGELTVRAKLVLPSPRKLQEAQEGTDQPSLHGOLCLVILAKNLPVRPDGTLNSFVGK 240
 Db 447 SNGELTVRAKLVLPSPRKLQEAQEGTDQPSLHGOLCLVILAKNLPVRPDGTLNSFVGK 506
 OY 241 CLTLPDQOKLRLKSPVLRKQACPOWKHSFVSGVTPAOLROSSLLELTVWDQALFGMNDRL 300
 Db 507 CLTLPDQOKLRLKSPVLRKQACPOWKHSFVSGVTPAOLROSSLLELTVWDQALFGMNDRL 566
 OY 301 LGTRLSKGDPTAVGGDACSLSKLOMOKVLSPLNMTDMLVLH 344
 Db 567 LGTRLSKGDPTAVGGDACSLSKLOMOKVLSPLNMTDMLVLH 610

RESULT 4

US-09-785-548-15
 ; Sequence 15, Application US/09785548
 ; Patent No. US20020155577A1
 ; GENERAL INFORMATION:
 ; APPLICANT: AVENTIS PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF P
 ; FILE REFERENCE: ST00005
 ; CURRENT APPLICATION NUMBER: US/09/785,548
 ; CURRENT FILING DATE: 2001-02-20
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 313
 ; TYPE: PRN
 ; ORGANISM: Homo sapiens
 US-09-785-548-15

Query Match 90.5%; Score 1640; DB 9; Length 313;
 Best Local Similarity 99.4%; Pred. No. 1.2e-159;
 Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 32 MGNFDNANVTGEIEFAIHCFKTHSLEICIKACKNLAYGEEKKKKCNPYKTYLLPDRSS 91
 Db 1 MGNFDNANVTGEIEFAIHCFKTHSLEICIKACKNLAYGEEKKKKCNPYKTYLLPDRSS 60
 OY 92 QGKRTGVQRTNVDPTFOETLKYQVAPAOVTRLOLVSVHMLGLTARVFLGEVYIISLAT 151
 Db 61 QGKRTGVQRTNVDPTFOETLKYQVAPAOVTRLOLVSVHMLGLTARVFLGEVYIISLAT 120
 OY 152 WDFEDSTQSRFMRHLRAKAEKEDSVPOSNGELTVRAKLVLPSPRKLQEAQEGTDPS 211
 Db 121 WDFEDSTQSRFMRHLRAKAEKEDSVPOSNGELTVRAKLVLPSPRKLQEAQEGTDPS 180
 OY 212 LHGOLCLVILAKNLPVRPDGTLNSFVGKCLTLPDQOKLRLKSPVLRKQACPOWKHSFV 271
 Db 181 LHGOLCLVILAKNLPVRPDGTLNSFVGKCLTLPDQOKLRLKSPVLRKQACPOWKHSFV 240
 OY 272 SGVTPAOLROSSLLELTVWDQALFGMNDRLGTRLSKGDPTAVGGDACSLSKLOMOKVLS 331
 Db 241 SGVTPAOLROSSLLELTVWDQALFGMNDRLGTRLSKGDPTAVGGDACSLSKLOMOKVLS 300
 OY 332 SPNMTDMLVLH 344
 Db 301 SPNMTDMLVLH 313


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RESULT 5
US-09-785-548-45
; Sequence 45, Application US/09785548
; Patent No. US20020155577A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF PARK
; FILE REFERENCE: ST000005
; CURRENT APPLICATION NUMBER: US/09/785,548
; CURRENT FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-785-548-45

Query Match          90.5%; Score 1640; DB 9; Length 313;
Best Local Similarity 99.4%; Pred. No. 1,2e-159;
Matches 311; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 32 MGNFDMANTGELIEFAIHCFKTHSLEICIKACKNLAYGEEKKKCNPYKTYLLPDRSS 91
1 MGNFDMANTGELIEFAIHCFKTHSLEICIKACKNLAYGEEKKKCNPYKTYLLPDRSS 60
QY 92 GSKRKTGVQRTVDPFQETLKYQVAPAOQVTRLOVSVHGLTARVFLGEVYISLAT 151
61 GSKRKTGVQRTVDPFQETLKYQVAPAOQVTRLOVSVHGLTARVFLGEVYISLAT 120
QY 152 WPEEDSTQSFRRHPLRAKAEKEDSVPOSNGELTVRAKLVLSRPRKLOAOGSTOOPS 211
121 WPEEDSTQSFRRHPLRAKAEKEDSVPOSNGELTVRAKLVLSRPRKLOAOGSTOOPS 180
DB 212 LHGQCLLVYLGAKNLPVRPBDGLNSFVKGCLTLPDQKRLKSFVLRKQACPCQKHSFEV 271
181 LHGQCLLVYLGAKNLPVRPBDGLNSFVKGCLTLPDQKRLKSFVLRKQACPCQKHSFEV 240
DB 272 SGVTPAQLQSSLELTVMDALFGMDRLIGSTRGSGGTAVGGDCSLKLOMOKVLS 331
241 SGVTPAQLQSSLELTVMDALFGMDRLIGSTRGSGGTAVGGDCSLKLOMOKVLS 300
QY 332 SPNLTMDMTLVLH 344
301 SPNLTMDMTLVLH 313
DB

RESULT 6
US-09-764-870-393
; Sequence 393, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 393
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (29)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (294)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (312)

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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (316)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (323)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (335)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-870-393

Query Match          68.1%; Score 1234; DB 10; Length 363;
Best Local Similarity 97.5%; Pred. No. 4.3e-118;
Matches 234; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ONLPSPAPSTIFSGGFRGSLISDSTCEMGNFDMANTGELIEFAIHCFKTHSLEIC 60
DB 124 ONLPSPAPSTIFSGGFRGSLISDSTCEMGNFDMANTGELIEFAIHCFKTHSLEIC 183
QY 61 IKACKNLAYGEEKKKCNPYKTYLLPDRSSOGKRTGVQRTVDPFQETLKYQVAPAQ 243
DB 184 IKACKNLAYGEEKKKCNPYKTYLLPDRSSOGKRTGVQRTVDPFQETLKYQVAPAQ 243
QY 121 LVTRLOVSVHGLTARVFLGEVYISLATWPEEDSTQSFRRHPLRAKAEKEDSVQ 180
DB 244 LVTRLOVSVHGLTARVFLGEVYISLATWPEEDSTQSFRRHPLRAKAEKEDSVQ 303
QY 181 SNGELTVRAKLVLSRPRKLOAOGSTOOPS LHGQCLLVYLGAKNLPVRPBDGLNSFVK 240
DB 304 SNGELTVRAKLVLSRPRKLOAOGSTOOPS LHGQCLLVYLGAKNLPVRPBDGLNSFVK 363

RESULT 7
US-09-764-870-502
; Sequence 502, Application US/09764870
; Patent No. US20020042386A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT214
; CURRENT APPLICATION NUMBER: US/09/764,870
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 502
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (22)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-870-502

Query Match          28.4%; Score 515; DB 10; Length 348;
Best Local Similarity 35.8%; Pred. No. 1.1e-44;
Matches 120; Conservative 62; Mismatches 119; Indels 34; Gaps 10;

QY 20 GSLISDSTCEMGNFDMANTGELIEFAIHCFKTHSLEICIKACKNLAYGEEKKKCN 79
DB 27 GSVMSVYS-----GDCGNLEVKGNIDPALEYVSLKELHFAVQCKDLAADVKKQSDP 81
QY 80 YKTYLLPDRSSOGKRTGVQRTVDPFQETLKYQVAPAOQVTRLOVSVHGLTAR 139
DB 82 YKATYLLPDRSSOGKRTGVQRTVDPFQETLKYQVAPAOQVTRLOVSVHGLTAR 141

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[illegible]

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OM protein - protein search, using sw model

Run on: January 31, 2003, 07:39:58 ; Search time 15 Seconds

(without alignments)
674.766 Million cell updates/sec

Title: US-09-785-548-2
Sequence: 1 QNLPSSAPSPRIFSGFRHG.....QMOKVLSPPNMTDVLVH 344

Scoring table: BLOSUM62

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Number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	211.5	11.7	422	3	US-08-872-979-8
2	179	9.9	355	3	US-08-872-979-7
3	176.5	9.7	425	4	US-09-036-315-2
4	174	9.6	1686	4	US-09-355-160D-2
5	173	9.5	375	3	US-08-872-979-3
6	170	9.4	137	2	US-08-609-049A-15
7	170	9.4	137	2	US-09-170-996-15
8	170	9.4	1658	2	US-08-609-049A-13
9	170	9.4	1658	4	US-09-170-996-13
10	170	9.4	1726	2	US-08-609-049A-30
11	170	9.4	1726	4	US-09-170-996-30
12	169	9.3	137	2	US-08-609-049A-14
13	169	9.3	137	4	US-09-170-996-14
14	169	9.3	425	4	US-09-036-315-5
15	169	9.3	1876	2	US-08-609-049A-12
16	169	9.3	1876	2	US-08-609-049A-28
17	169	9.3	1876	4	US-09-170-996-12
18	169	9.3	1876	4	US-09-170-996-38
19	135.5	7.5	113	4	US-09-036-315-10
20	132	7.3	140	2	US-08-609-049A-16
21	132	7.3	140	4	US-09-170-996-16
22	128.5	7.1	120	4	US-09-036-315-9
23	122	6.7	117	4	US-09-036-315-6
24	120	6.6	136	2	US-08-609-049A-18
25	120	6.6	136	4	US-09-170-996-18
26	120	6.6	138	2	US-08-609-049A-17
27	120	6.6	138	4	US-09-170-996-17

28	120	6.6	671	6	5266464-2
29	117.5	6.5	115	4	US-09-036-315-8
30	86	4.7	1148	2	US-08-313-185-58
31	86	4.7	1148	3	US-09-082-614A-58
32	84	4.6	756	2	US-08-887-518-4
33	84	4.6	756	2	US-09-023-321-4
34	84	4.6	756	2	US-08-890-853-2
35	84	4.6	756	2	US-09-032-475-4
36	84	4.6	756	2	US-09-099-125A-2
37	84	4.6	756	2	US-09-099-124A-2
38	84	4.6	756	4	US-09-032-476-2
39	84	4.6	756	4	US-08-890-854-2
40	84	4.6	756	4	US-09-023-324-2
41	84	4.6	756	4	US-09-168-629-15
42	84	4.6	756	4	US-08-910-820-9
43	83.5	4.6	1019	1	US-08-271-364A-7
44	83.5	4.6	1019	2	US-08-222-715B-26
45	83	4.6	240	2	US-08-738-367-7

ALIGNMENTS

RESULT 1
US-08-872-979-8
Sequence 8, Application US/08872979
Patent No. 6074844
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: TWO NEW HUMAN MEMBRANE FUSION PROTEINS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,979
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0320 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 338658
US-08-872-979-8
Query Match 11.7%; Score 211.5; DB 3; Length 422;
Best Local Similarity 25.5%; Pred. No. 5.2e-15;

